

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 19:21:17 ; Search time 27.3991 Seconds  
(without alignment)  
275.930 Million cell updates/sec

Title: US-10-044-896-3

Perfect score: 594  
Sequence: 1 DIQWQSPSLASVSDRVT.....SWGIRFGQGTKEIKRTV 114

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PTUS COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	509	85.7	130	1 US-08-137-117D-86	Sequence 86, Appl
2	509	85.7	130	2 US-08-436-717-86	Sequence 86, Appl
3	490	82.5	218	5 PCT-US96-13152-2	Sequence 2, Appl
4	487	82.0	109	3 US-09-157-370-3	Sequence 3, Appl
5	486	81.8	114	2 US-08-887-352B-9	Sequence 9, Appl
6	486	81.8	114	2 US-08-887-352B-10	Sequence 10, Appl
7	486	81.8	114	3 US-09-109-207C-10	Sequence 10, Appl
8	486	81.8	114	3 US-09-296-005-10	Sequence 10, Appl
9	486	81.8	114	4 US-09-920-171-10	Sequence 10, Appl
10	486	81.8	114	4 US-08-716-028-10	Sequence 10, Appl
11	486	81.8	114	4 US-10-113-996-10	Sequence 10, Appl
12	486	81.8	218	2 US-08-887-352B-13	Sequence 13, Appl
13	486	81.8	218	3 US-08-466-151-9	Sequence 9, Appl
14	486	81.8	218	3 US-09-109-207C-13	Sequence 13, Appl
15	486	81.8	218	3 US-09-296-005-13	Sequence 13, Appl
16	486	81.8	218	3 US-08-466-153B-9	Sequence 9, Appl
17	486	81.8	218	4 US-09-920-171-13	Sequence 13, Appl
18	486	81.8	218	4 US-08-887-352B-9	Sequence 9, Appl
19	486	81.8	218	4 US-09-802-077-9	Sequence 9, Appl
20	486	81.8	218	4 US-09-716-028-13	Sequence 13, Appl
21	486	81.8	218	4 US-10-113-996-13	Sequence 13, Appl
22	483	81.3	114	3 US-09-109-207C-9	Sequence 9, Appl
23	483	81.3	114	3 US-08-286-005-9	Sequence 9, Appl
24	483	81.3	114	4 US-09-920-171-9	Sequence 9, Appl
25	483	81.3	114	4 US-09-716-028-9	Sequence 9, Appl
26	483	81.3	114	4 US-10-113-996-9	Sequence 9, Appl
27	483	81.3	240	4 US-09-192-854-2	Sequence 2, Appl

28	481	81.0	111	2 US-08-887-352B-7	Sequence 7, Appl
29	481	81.0	111	3 US-09-109-207C-7	Sequence 7, Appl
30	481	81.0	111	3 US-09-286-005-7	Sequence 7, Appl
31	481	81.0	111	4 US-09-920-171-7	Sequence 7, Appl
32	481	81.0	111	4 US-09-716-028-7	Sequence 7, Appl
33	481	81.0	111	4 US-10-113-996-7	Sequence 17, Appl
34	480.5	80.9	110	3 US-09-672-609-17	Sequence 17, Appl
35	480.5	80.9	110	4 US-09-025-403A-17	Sequence 15, Appl
36	477.5	80.4	110	3 US-09-025-403A-15	Sequence 15, Appl
37	477.5	80.4	110	4 US-08-887-352B-8	Sequence 8, Appl
38	477	80.3	218	3 US-09-282-505-1	Sequence 1, Appl
39	477	80.3	218	3 US-09-054-255-1	Sequence 1, Appl
40	477	80.3	218	4 US-09-282-846-1	Sequence 1, Appl
41	477	80.3	218	4 US-09-680-145-1	Sequence 1, Appl
42	477	80.3	218	4 US-09-483-588-1	Sequence 1, Appl
43	476	80.1	131	3 US-08-579-378A-18	Sequence 18, Appl
44	476	80.1	214	2 US-07-934-373C-39	Sequence 39, Appl
45	475	80.0			

## ALIGNMENTS

RESULT 1  
US-08-137-117D-86  
; Sequence 86, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117D  
; FILING DATE: 20-DEC-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELER: 904136  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 130 amino acids  
; TYPE: amino acid

partial identity No 8, context # 9

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-86

Query Match 85.7%; Score 509; DB 1; Length 130;  
Best Local Similarity 90.1%; Pred. No. 2,7e-40;  
Matches 100; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHWTQOKPGKAPKVLISYASNTLS 60  
DB 20 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHWTQOKPGKAPKVLISYASNTLS 79

QY 61 GVPSPRSGSGSGTDFLTITSSLOPEDFATYYCOHSGWGIPTFGQTKVEIK 111  
DB 80 GVPSPRSGSGSGTDFLTITSSLOPEDFATYYCOHSGWGIPTFGQTKVEIK 130

## RESULT 2

US-08-436-717-86  
Sequence 86, Application US/08436717  
Patent No. 5817790

## GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:  
CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399

## TELEX: 904136

INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-436-717-86

Query Match 85.7%; Score 509; DB 2; Length 130;  
Best Local Similarity 90.1%; Pred. No. 2,7e-40;  
Matches 100; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHWTQOKPGKAPKVLISYASNTLS 60  
DB 20 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHWTQOKPGKAPKVLISYASNTLS 79

QY 61 GVPSPRSGSGSGTDFLTITSSLOPEDFATYYCOHSGWGIPTFGQTKVEIK 111  
DB 80 GVPSPRSGSGSGTDFLTITSSLOPEDFATYYCOHSGWGIPTFGQTKVEIK 130

## RESULT 3

PCT-US96-13152-2  
Sequence 2, Application PC/TUS9613152

## GENERAL INFORMATION:

APPLICANT: Martin, Ulrich, et al.  
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fail  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Felte & Lynch  
ADDRESSER: Attn: Norman D. Hanson  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/13152  
FILING DATE:  
CLASSIFICATION:

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953  
FILING DATE: 27-Dec-95  
APPLICATION NUMBER: EP 95 112 895.8  
FILING DATE: 17-Aug-95  
APPLICATION NUMBER: EP 95 114 969.9  
FILING DATE: 19-Sep-95  
ATTORNEY/AGENT INFORMATION:  
NAME: Norman D. Hanson

## REGISTRATION NUMBER: 30,946

## REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PPE/NDH

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-13152-2

Query Match 82.5%; Score 490; DB 5; Length 218;  
Best Local Similarity 86.0%; Pred. No. 2,9e-38;  
Matches 98; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHWTQOKPGKAPKVLISYASNTLS 60  
DB 1 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHWTQOKPGKAPKVLISYASNTLS 60

QY 61 GVPSPRSGSGSGTDFLTITSSLOPEDFATYYCOHSGWGIPTFGQTKVEIKRTV 114  
DB 61 GVPSPRSGSGSGTDFLTITSSLOPEDFATYYCOHSGWGIPTFGQTKVEIKRTV 114

RESULT 4  
US-09-157-370-3  
; Sequence 3, Application US/09157370A  
; Patent No. 6262238  
; GENERAL INFORMATION:  
; APPLICANT: STEIER, Boris  
; APPLICANT: STEINBACHER, Stefan  
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES  
; FILE REFERENCE: P9341-8072  
; CURRENT APPLICATION NUMBER: US/09/157,370A  
; EARLIER FILING DATE: 1998-09-21  
; EARLIER APPLICATION NUMBER: 08/765,179  
; EARLIER FILING DATE: 1997-01-14  
; EARLIER APPLICATION NUMBER: PCT/EP95/02626  
; EARLIER FILING DATE: 1995-07-06  
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7  
; EARLIER FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-157-370-3

Query Match 82.0%; Score 487; DB 3; Length 109;  
Best Local Similarity 85.8%; Pred. No. 2.5e-38;  
Matches 97; Conservative 5; Mismatches 7; Indels 4; Gaps 1;

Qy 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISVSNLES 60  
Db 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISVSNLES 56

Qy 61 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCOHSMGIPRTFGGTVEIKRTV 113  
Db 57 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCOHSMGIPRTFGGTVEIKRTV 109

RESULT 5  
US-08-887-352B-9  
; Sequence 9, Application US/0887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids

TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-887-352B-9

Query Match 81.8%; Score 486; DB 2; Length 114;  
Best Local Similarity 86.0%; Pred. No. 3.2e-38;  
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISVSNLES 60  
Db 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISVSNLES 60

Qy 61 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCOHSMGIPRTFGGTVEIKRTV 114  
Db 61 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCOHSMGIPRTFGGTVEIKRTV 114

RESULT 6  
US-08-887-352B-10  
; Sequence 10, Application US/0887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-10

Query Match 81.8%; Score 486; DB 2; Length 114;  
Best Local Similarity 86.0%; Pred. No. 3.2e-38;  
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISVSNLES 60  
Db 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISVSNLES 60

Qy 61 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCOHSMGIPRTFGGTVEIKRTV 114  
Db 61 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCOHSMGIPRTFGGTVEIKRTV 114

RESULT 7  
US-09-109-207C-10  
; Sequence 10, Application US/09109207C  
; Patent No. 6172213

```
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
/ FILE REFERENCE: P1123R1
/ CURRENT APPLICATION NUMBER: US/09/109,207C
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/051,554
/ PRIOR FILING DATE: 1997-07-03
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-10
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Query Match      81.8%; Score 486; DB 3; Length 114;
Best Local Similarity 86.0%; Pred. No. 3,2e-38;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
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QY 1 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNTLS 60
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Db 1 DIQMTSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNMYQOKPGKAPKLLIYAASYLE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVPSRFGSGSGGTDFTLTISLQPEDPATYTCQSHEDPYTFQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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## RESULT 8

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US-09-296-005-10
/ Sequence 10, Application US/09296005
/ Patent No. 6290957
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
/ FILE REFERENCE: P1123C1r
/ CURRENT APPLICATION NUMBER: US/09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ EARLIER APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ NUMBER OF SEQ ID NOS: 26
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-10
```

```
Query Match      81.8%; Score 486; DB 3; Length 114;
Best Local Similarity 86.0%; Pred. No. 3,2e-38;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
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```
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Db 1 DIQMTSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNMYQOKPGKAPKLLIYAASYLE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVPSRFGSGSGGTDFTLTISLQPEDPATYTCQSHEDPYTFQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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## RESULT 9

```
US-09-920-171-10
/ Sequence 10, Application US/09920171
/ Patent No. 6682735
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
/ FILE REFERENCE: P1123C2US
/ CURRENT APPLICATION NUMBER: US/09/920,171
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-10
```

```
Query Match      81.8%; Score 486; DB 4; Length 114;
Best Local Similarity 86.0%; Pred. No. 3,2e-38;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
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QY 1 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNTLS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNMYQOKPGKAPKLLIYAASYLE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVPSRFGSGSGGTDFTLTISLQPEDPATYTCQSHEDPYTFQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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## RESULT 10

```
US-09-716-028-10
/ Sequence 10, Application US/09716028
/ Patent No. 6723833
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
/ FILE REFERENCE: P1123R1
/ CURRENT APPLICATION NUMBER: US/09/716,028
/ PRIOR FILING DATE: 2000-11-17
/ PRIOR APPLICATION NUMBER: US 09/109,207
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/051,554
/ PRIOR FILING DATE: 1997-07-03
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-716-028-10
```

```
Query Match      81.8%; Score 486; DB 4; Length 114;
Best Local Similarity 86.0%; Pred. No. 3,2e-38;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNTLS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNMYQOKPGKAPKLLIYAASYLE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 61 GVPSRFGSGSGGTDFTLTISLQPEDPATYTCQSHEDPYTFQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GVPSRFGSGSGGTDFTLTISLQPEDPATYTCQSHEDPYTFQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

## RESULT 11



US-10-113-996-10  
; Sequence 10, Application US/10113996  
; Patent No. 6761889  
; GENERAL INFORMATION:  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies  
; FILE REFERENCE: P1123C3US  
; CURRENT APPLICATION NUMBER: US/10/113,996  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: US 08/887,352  
; PRIOR FILING DATE: 1997-07-02  
; PRIOR APPLICATION NUMBER: US 09/296,005  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: US 09/920,171  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 10  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-10-113-996-10  
  
Query Match 81.8%; Score 486; DB 4; Length 114;  
Best Local Similarity 86.0%; Pred. No. 3,2e-38;  
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;  
  
Qy 1 DIQWTQSPSSISASVGVGRVITTCRASQSVSTSSYSYMWYQKKGKAPKVLISYASNI 60  
Db 1 DIQWTQSPSSISASVGVGRVITTCRASQSVSDYDGSYMWYQKKGKAPKVLISYASNI 60  
61 GVPSRFSGSGSGTDFTLTISLSLPEDPATYTCQHSWGIPRTFGGTVEIKRTV 114  
61 GVPSRFSGSGSGTDFTLTISLSLPEDPATYTCQSHDEPTFGGTVEIKRTV 114  
Db 61 GVPSRFSGSGSGTDFTLTISLSLPEDPATYTCQSHDEPTFGGTVEIKRTV 114  
  
RESULT 12  
US-08-887-352B-13  
; Sequence 13, Application US/0887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatlin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/952-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-13  
  
Query Match 81.8%; Score 486; DB 2; Length 218;  
Best Local Similarity 86.0%; Pred. No. 6,8e-38;  
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;  
  
Qy 1 DIQWTQSPSSISASVGVGRVITTCRASQSVSTSSYSYMWYQKKGKAPKVLISYASNI 60  
Db 1 DIQWTQSPSSISASVGVGRVITTCRASQSVSDYDGSYMWYQKKGKAPKVLISYASNI 60  
61 GVPSRFSGSGSGTDFTLTISLSLPEDPATYTCQHSWGIPRTFGGTVEIKRTV 114  
61 GVPSRFSGSGSGTDFTLTISLSLPEDPATYTCQSHDEPTFGGTVEIKRTV 114  
Db 61 GVPSRFSGSGSGTDFTLTISLSLPEDPATYTCQSHDEPTFGGTVEIKRTV 114  
  
RESULT 13  
US-08-466-151-9  
; Sequence 9, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatlin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,151  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466163  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: 08/405617  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/185899  
; FILING DATE: 26-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/879495  
; FILING DATE: 07-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-466-151-9  
  
Query Match 81.8%; Score 486; DB 3; Length 218;



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OM protein - protein search, using sw model

Run on: December 29, 2004, 18:59:15 ; Search time 117.425 Seconds  
(without alignments)  
348.266 Million cell updates/sec

Title: US-10-044-896-3

Perfect score: 594  
Sequence: 1 DIQWTQSPSSLSASVGDRTV.....SMGIPTFGQCTKYIKRTV 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Genesepc\_23Sep04:\*

1: genesepc1980s:\*\n2: genesepc1990s:\*\n3: genesepc2000s:\*\n4: genesepc2001s:\*\n5: genesepc2002s:\*\n6: genesepc2003as:\*\n7: genesepc2003bs:\*\n8: genesepc2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	594	100.0	114 5 AAE28148	AAE28148 Humanised
2	501	84.3	111 2 AAR85242	AAR85242 Humanised
3	494	83.2	218 5 AAM49204	AAM49204 Humanised
4	493	83.0	132 2 AAW22842	AAW22842 Human ant
5	490	82.5	218 5 AAM13563	AAM13563 Humanised
6	489	82.3	108 6 ABP96011	ABP96011 HSA antib
7	489	82.3	108 8 ADL92462	ADL92462 Single do
8	489	82.3	238 3 AAW90930	AAW90930 Humanised
9	489	82.3	238 5 ABB74899	ABB74899 Humanised
10	488	82.2	238 3 AAW90932	AAW90932 Humanised
11	488	82.2	238 5 ABB74901	ABB74901 Humanised
12	488	82.2	240 4 AAB45995	AAB45995 Human MUC
13	486	81.8	114 2 AAM13922	AAM13922 light cha
14	486	81.8	114 2 AAW95654	AAW95654 Mus muscu
15	486	81.8	114 2 AAW95655	AAW95655 Mus muscu
16	486	81.8	114 4 AAB76944	AAB76944 Variable
17	486	81.8	114 8 ADN07031	ADN07031 Anti-IGE
18	486	81.8	218 4 AAW95658	AAW95658 Mus muscu
19	486	81.8	218 4 AAY85200	AAY85200 light cha
20	486	81.8	218 4 AAB76947	AAB76947 Full vari
21	486	81.8	218 8 ADN07034	ADN07034 Anti-IGS
22	486	81.8	240 4 AAB45996	AAB45996 Human MUC
23	485	81.6	238 3 AAW90931	AAW90931 Humanised
24	485	81.6	238 5 ABB74900	ABB74900 Humanised
25	484	81.5	233 8 ADL93655	ADL93655 Human CD4

26	484	81.5	240 4 AAB46010	AAB46010 Human MUC
27	483	81.3	108 6 ABP96009	ABP96009 HSA antib
28	483	81.3	108 7 ADL91345	ADL91345 VL chain
29	483	81.3	108 8 ADL92386	ADL92386 Anti-HSA
30	483	81.3	108 8 ADO36372	ADO36372 Intracell
31	483	81.3	114 4 AAB76943	AAB76943 Variable
32	483	81.3	114 8 ADN07030	ADN07030 Anti-IGS
33	483	81.3	219 8 ADN07066	ADN07066 F(ab)-pha
34	483	81.3	240 2 AAY02472	AAY02472 A single
35	483	81.3	240 4 AAB46007	AAB46007 Human MUC
36	483	81.3	240 4 AAB46038	AAB46038 Human Tr
37	483	81.3	240 4 AAB46008	AAB46008 Human MUC
38	483	81.3	240 4 AAB46006	AAB46006 Human MUC
39	483	81.3	240 4 AAB46005	AAB46005 Human MUC
40	483	81.3	240 4 AAB45994	AAB45994 Human MUC
41	483	81.3	240 6 ABP95997	ABP95997 Human ser
42	483	81.3	240 6 ABB38594	ABB38594 Hepatitis
43	483	81.3	240 8 ADL92369	ADL92369 Human pha
44	482	81.1	108 6 ABP96010	ABP96010 HSA antib
45	482	81.1	108 8 ADL92461	ADL92461 Single do

## ALIGNMENTS

RESULT 1	AAE28148	AAE28148 standard; protein, 114 AA.
XX	AAE28148;	
AC		
XX		
DT	27-DEC-2002	(first entry)
XX		
DE	Humanised 9F3 version 13 (V13) light chain variable domain.	
XX		
KW	Human; interferon alpha; IFNalpha; insulin-dependent diabetes mellitus;	
KW	autoimmune disease; systemic lupus erythematosus; autoimmune thyroiditis;	
KW	antibody therapy; immunosuppressive; antiinflammatory; dermatological;	
KW	9F3 monoclonal antibody; light chain variable domain.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	Region	24..38
FT	/note= "Complementarity determining region 1 (CDR1)"	
FT	Region	54..60
FT	/note= "Complementarity determining region 2 (CDR2)"	
FT	Region	93..102
FT	/note= "Complementarity determining region 3 (CDR3)"	
XX		
PD	29-AUG-2002.	WO200266649-A2.
XX		
PR	29-JAN-2002; 2002WO-US002709.	
XX		
PR	22-FEB-2001; 2001US-0270775P.	
XX		
PR	09-JAN-2002; 2002US-00044896.	
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Chuntarapai A, Kim JK, Presta LG, Stewart T,	
XX		
DR	WPI; 2002-682767/73.	
XX		
PT	New anti-interferon alpha monoclonal antibody, 9F3, useful for treating	
PT	autoimmune diseases e.g. insulin-dependent diabetes mellitus, systemic	
PT	lupus erythematosus and autoimmune thyroiditis.	
XX		
PS	Disclosure; Page 97; 100p; English.	
XX		
CC	The present invention relates to novel anti-interferon alpha (IFNalpha)	

CC	monoclonal antibody, 9F3 which binds to and neutralises a biological
CC	activity of IFN-alpha subtypes. The anti-IFNalpha monoclonal antibodies
CC	of the invention are useful for treating autoimmune diseases such as
CC	insulin-dependent diabetes mellitus, systemic lupus erythematosus and
CC	autoimmune thyroiditis. They are useful as reagents in diagnostic assays
CC	for IFN-alpha expression, for the affinity purification of various IFN-
CC	alpha subtypes from recombinant cell culture or natural resources and for
CC	the detection of IFN-alpha in diagnostic assay methods. Sequences of the
CC	invention are also useful in antibody therapy. The present sequence is
CC	anti-human IFNalpha monoclonal antibody 9F3 version 13 (V13) light chain
CC	variable domain
SQ	Sequence 114 AA;
QY	Query Match            100.0%; Score 594; DB 5; Length 114; Best Local Similarity    100.0%; Pred. No. 2.9e-32; Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 DIQMTOGSSSLASAVGDRTVTTCRASGVSTSYSMVMYQKPKAKRVLIYSANLES 60   1 DIQMTOGSSSLASAVGDRTVTTCRASGVSTSYSMVMYQKPKAKRVLIYSANLES 60
OY	61 GVPRPFGSGSGGTFTLTITSILOPEDFATYYCOHSMWGIPRTFGQTKYEIKRTV 114   61 GVPRPFGSGSGGTFTLTITSILOPEDFATYYCOHSMWGIPRTFGQTKYEIKRTV 114
ID	AAR85242 standard; protein; 111 AA.
AC	AAR85242;
XX	
D7	09-APR-1996 (first entry)
DE	Humanised antibody variable light chain region (VZV HUvX).
XX	
KW	Antibody; varicella zoster virus; Ab; VSV; treatment; prevention;
KM	Infection; detection; isolation; monoclonal antibody; MBd; mimetic;
KW	humanised; murine; heavy chain; light chain; variable region; CDR; NEWM;
XX	REF.
OS	Synthetic.
PN	MO95J1546-A1.
PD	23-NOV-1995.
PF	28-APR-1995; 95WO-US0005305.
XX	
PR	28-APR-1994; 94US-00234133.
PA	(SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
FL	Moses MT, Wallace TP, Carr FU, Harris WJ;
DR	WP1; 1996-010932/O1.
PT	Varicella zoster virus gpIII antibody with humanised variable region -
PT	for treatment, prevention or diagnosis of varicella zoster virus
XX	infections.
PS	Claim 7; Page 31; 58pp; English.
CC	Antibodies (Ab) comprising a humanised variable region specifically
CC	binding to a varicella zoster virus (VZV) can be used to treat or prevent
CC	VZV infection. They may optionally be attached to a therapeutic agent.
CC	They may also be used, when labelled, to detect VZV particles and
CC	infected cells in blood; for the removal/neutralisation of infectious
CC	VZV in blood; for the selection/isolation of human monoclonal Abs and
CC	for the design of (non-)peptide mimetics with similar diagnostic and
CC	therapeutic uses. The variable region CDR portion is derived from murine
CC	Ab 206 and the heavy and light chain variable region frameworks are NEMM

[illegible]

PR 01-SEP-2000; 2000US-0229933P.  
PR 16-MAR-2001; 2001US-0276452P.  
XX  
XX (BIOJ ) BIOGEN INC.  
XX  
XX Karpusas M, Hsu Y, Taylor FR, Zheng Z;  
XX WPI; 2002-329760/36.  
DR  
XX  
PT Crystal comprising a CD154 polypeptide complexed with an anti-CD154  
PT antibody, or its antigen binding fragment, useful for designing drugs for  
PT the treatment of an autoimmune disease, an allergy, multiple sclerosis  
PT and Alzheimer's disease.  
XX  
XX  
XX Example 1; Fig 8; 470pp; English.  
XX  
XX The invention relates to a crystal comprising a CD145 polypeptide in  
XX complex with an anti-CD45 antibody or its antigen-binding fragment, and  
XX the structure coordinates of such a crystal. In particular, the crystal  
XX comprises human CD145 (AAW49202) and a humanised version of the murine  
XX monoclonal antibody 5c8 (hu5c8; AAW49203, AAW49204). CD145, also known as  
XX CD40L, gp39, T-BAM, 5c8 antigen, CD40CR and TRAP) is a 32 kD type II  
XX membrane glycoprotein which is transiently expressed on activated T  
XX cells. It interacts with CD40 which is expressed on mature B cells,  
XX macrophages, dendritic cells, fibroblasts and activated endothelial  
XX cells. This CD40:CD145 interaction is required for T cell-dependent  
XX antibody responses, type I T-helper cell responses, and nitric oxide (NO)  
XX production by macrophages. NO mediates many of the pro-inflammatory  
XX activities of macrophages, and disruption of the CD40:CD145 interaction  
XX via the use of an anti-CD145 antibody has been shown to reduce the  
XX symptoms of autoimmune and inflammatory conditions. The crystal structure  
XX of the invention can be used to determine the three dimensional structure  
XX of the CD145:anti-CD145 antibody complex, and thereby provide information  
XX about this interaction which may be of use in designing non-antibody  
XX CD145 agonists and antagonists which modulate the CD40:CD145 interaction.  
XX Such compounds may be used in the treatment of an unwanted immune  
XX response, an unwanted inflammatory response, an autoimmune disease, an  
XX allergy, an inhibitor response to a therapeutic agent, rejection of a  
XX donor organ, or a B cell cancer. They may be specifically be used to  
XX treat systemic lupus erythematosus, lupus nephritis, lupus neuritis,  
XX asthma, chronic obstructive pulmonary disease (COPD), bronchitis,  
XX emphysema, multiple sclerosis, uveitis, Alzheimer's disease, traumatic  
XX spinal cord injury, stroke, atherosclerosis, coronary restenosis,  
XX ischaemic congestive heart failure, cirrhosis, hepatitis C, diabetic  
XX neuropathy, glomerulonephritis, osteoarthritis, rheumatoid arthritis,  
XX psoriasis, atopic dermatitis, systemic sclerosis, radiation-induced  
XX fibrosis, Crohn's disease, ulcerative colitis, multiple myeloma and  
XX cachexia. Sequences AAW49203 and AAW49204 represent, respectively, the  
XX heavy and light chains of the humanised version of the murine monoclonal  
XX antibody 5c8 (hu5c8). (Updated on 23-AUG-2003 to standardise OS field)  
XX  
SQ Sequence 218 AA;  
Query Match 83.2%; Score 494; DB 5; Length 218;  
Best Local Similarity 79.8%; Pred. No. 2e-25;  
Matches 91; Conservative 13; Mismatches 10; Indels 0; Gaps 0;  
QY 1 DIQWTGSSSLASVGVGRVITTCRASQSVSTSSYSYMWYQKRGKAPKVLISYASNL60  
DB 1 DIVLTQSPATLSVSPERATISCRASQSVSTSSYSYMWYQKRGKAPKVLISYASNL60  
QY 61 GVPBRFSGSSGSDPFTLTISLQPEDPATYTCQHSKGIPTFGGTVEIKRTV 114  
DB 61 GVPBRFSGSSGSDPFTLTISLQPEDPATYTCQHSKGIPTFGGTVEIKRTV 114  
RESULT 4  
ID AAW22842 standard; protein: 132 AA.  
XX  
XX AAW22842;  
XX  
DT 12-SEP-1997 (first entry)

XX  
DE Human anti-tumour antigen antibody light chain variable region.  
XX  
XX Human; tumour antigen; cancer; monoclonal; antibody; light chain;  
XX variable region; medicine; pharmacology; biochemistry; CDR;  
XX complementarity determining region.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..22  
XX /label= sig\_peptide  
XX Peptide 23..132  
XX /label= mat\_peptide  
XX FT 46..56  
XX /label= CDR\_1  
XX FT 72..78  
XX /label= CDR\_2  
XX FT 111..119  
XX /label= CDR\_3  
XX  
XX JP09100300-A.  
XX  
XX 15-APR-1997.  
XX  
XX 03-OCT-1995; 95JP-00278266.  
XX  
XX 03-OCT-1995; 95JP-00278266.  
XX  
XX (HAGI/) HAGIMARA Y.  
XX  
XX WPI: 1997-276726/25.  
XX  
XX N-PSDB; AAT75423.  
XX  
XX Anticancer human monoclonal antibody variable region sequences - and  
XX related DNA and RNA.  
XX  
XX  
XX Claim 9; Page 11; 14pp; Japanese.  
XX  
XX The present sequence is a human anti-tumour antigen monoclonal antibody  
XX (Mab) light chain variable region, useful in medicine, pharmacology and  
XX biotechnology. The isotype of a Mab secreted by the human/human hybridoma  
XX HT was determined to be mu and kappa. Human Mab was purified, and the  
XX antigen recognised by human Mab C1N-1gM identified by western blotting  
XX  
SQ Sequence 132 AA;  
Query Match 83.0%; Score 493; DB 2; Length 132;  
Best Local Similarity 85.1%; Pred. No. 1.6e-25;  
Matches 97; Conservative 8; Mismatches 5; Indels 4; Gaps 1;  
QY 1 DIQWTGSSSLASVGVGRVITTCRASQSVSTSSYSYMWYQKRGKAPKVLISYASNL60  
DB 23 DIQWTGSSSLASVGVGRVITTCRASQSVSTSSYSYMWYQKRGKAPKVLISYASNL60  
QY 61 GVPBRFSGSSGSDPFTLTISLQPEDPATYTCQHSKGIPTFGGTVEIKRTV 114  
DB 79 GVPBRFSGSSGSDPFTLTISLQPEDPATYTCQHSKGIPTFGGTVEIKRTV 132  
RESULT 5  
ID AAW13563 standard; protein: 218 AA.  
XX  
XX AAW13563;  
XX  
XX 17-OCT-2003 (revised)  
XX DT 03-JUN-1997 (first entry)  
XX  
XX Humanised anti-L-selectin antibody HuDreg 55 light chain.  
XX  
XX L-selectin; humanised antibody; HuDreg 55; acute organ damage;  
XX organ failure; poly-trauma; haemorrhagic-traumatic shock.  
XX

XX Mus; sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX WO9706822-A1.  
 XX 27-FEB-1997.  
 XX 27-FEB-1997.  
 XX 14-AUG-1996; 96WO-US013152.  
 XX 17-AUG-1995; 95EP-00112895.  
 XX 19-SEP-1995; 95EP-00114696.  
 XX 27-DEC-1995; 95US-00578953.  
 XX (PROT-) PROTEIN DESIGN LABS INC.  
 PA (BOE) BOEHRINGER MANNHEIM GMBH.  
 XX Haselbeck A, Schumacher G, Co M, Martin U;  
 PI WPI; 1997-165036/15.  
 DR N-PSDB; AAT61280.  
 XX Using anti-selectin antibody to prevent acute organ damage and multiple  
 PT organ failure - during extracorporeal circulation or following  
 PT polycrma, e. g. haemorrhagic-traumatic shock.  
 XX Disclosure; Page 32-33; 52pp; English.  
 XX Humanised anti-L-selectin antibody Hudreg 55 comprises 2 light chains  
 CC each having the sequence given in AAW13563 and 2 heavy chains each having  
 CC the sequence given in AAW13564. These are encoded by the cDNA clones  
 CC given in AAW61280 and AAW1281. Hudreg 55 can be used to prevent multiple  
 CC organ failure associated with polycrma and for the prevention of acute  
 CC organ damage associated with extracorporeal blood circulation. The  
 CC antibody inhibits interaction between the carbohydrate-recognising domain  
 CC of the selectin and the corresponding cell surface receptor. (Updated on  
 CC 17-OCT-2003 to standardise OS field)  
 XX SQ Sequence 218 AA;  
 Query Match 82.5%; Score 490; DB 2; Length 218;  
 Best Local Similarity 86.0%; Pred. No. 3.7e-25;  
 Matches 98; Conservative 4; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQSVTSYVMHWYQOKRGA PKYLISYASNTLS 60  
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQSVTDGSDYNNMWYQOKRGA PKYLISYASNTLS 60  
 QY 61 GVSRRFGSGSGGTDFTLTISSLQPEDPATYVCOHSMGIPRTFGQTKVEIKR 114  
 DB 61 GVSRRFGSGSGGTDFTLTISSLQPEDPATYVCOHSMGIPRTFGQTKVEIKR 114  
 RESULT 6  
 ABP96011 ID ABP96011 standard; protein; 108 AA.  
 AC ABP96011;  
 DT 01-MAY-2003 (first entry)  
 XX HSA antibody related V kappa chain E55d.  
 DE HSA antibody related V kappa chain E55d.  
 XX Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV;  
 KW antiinflammatory; antianemic; immunosuppressive; neuroprotective;  
 KW dual-specific ligand; cancer; HIV infection; hepatitis; rubella; anaemia;  
 KW inflammation; autoimmune disorder; multiple sclerosis; Crohn's disease;  
 KW myasthenia gravis.  
 XX Homo sapiens.  
 OS Synthetic.

PN WO2003002609-A2.  
 XX 09-JAN-2003.  
 PD 28-JUN-2002; 2002WO-GB003014.  
 XX 28-JUN-2001; 2001GB-00015841.  
 XX (MED1-) MEDICAL RES COUNCIL.  
 PA Winter G, Ignatovich O, Tomlinson I;  
 PI WPI; 2003-210246/20.  
 DR Dual-specific ligand having immunoglobulins with binding specificity to  
 XX different antigens or epitopes, useful for treating, preventing or  
 PT diagnosing diseases, e.g. cancer, HIV infection, inflammations, or  
 PT myasthenia gravis.  
 XX Example 1; Fig 3; 84pp; English.  
 PS The present invention describes a dual-specific ligand (I) comprising:  
 CC (a) a first single immunoglobulin variable domain with a binding  
 CC specificity to a first antigen or epitope; and (b) a second complementary  
 CC immunoglobulin single variable domain with a binding activity to a second  
 CC antigen or epitope. The binding domains are mutually complementary, and  
 CC the first and second domains lack mutually complementary domains that  
 CC share the same specificity. (I) has cytostatic, anti-HIV, antianemic,  
 CC antiinflammatory, immunosuppressive and neuroprotective activities. The  
 CC dual-specific ligand is useful for treating, preventing or diagnosing  
 CC diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,  
 CC inflammations or autoimmune disorders (e.g. multiple sclerosis, Crohn's  
 CC disease or myasthenia gravis). The dual-specific ligand may be used to  
 CC recruit cytotoxic T-cells to a cancer cell. The dual-specific ligand is  
 CC also useful for monitoring the efficacy of drugs, as well as for  
 CC monitoring toxicity. The present sequence represents a human serum  
 CC albumin (HSA) related antibody V kappa sequence, which is used in an  
 CC example from the present invention  
 XX SQ Sequence 108 AA;  
 Query Match 82.3%; Score 489; DB 6; Length 108;  
 Best Local Similarity 85.7%; Pred. No. 2.4e-25;  
 Matches 96; Conservative 6; Mismatches 6; Indels 4; Gaps 1;  
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQSVTSYVMHWYQOKRGA PKYLISYASNTLS 60  
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQSVS---STLNMWYQOKRGA PKYLISYASNTLS 56  
 QY 61 GVSRRFGSGSGGTDFTLTISSLQPEDPATYVCOHSMGIPRTFGQTKVEIKR 112  
 DB 57 GVSRRFGSGSGGTDFTLTISSLQPEDPATYVCOHSMGIPRTFGQTKVEIKR 108  
 RESULT 7  
 ADL92462 ID ADL92462 standard; protein; 108 AA.  
 AC ADL92462;  
 DT 20-MAY-2004 (first entry)  
 XX Single domain antibody-related light chain variable region E55d protein.  
 DE Single domain antibody-related light chain variable region E55d protein.  
 XX immunoglobulin single variable domain; cytostatic; antiinflammatory;  
 KW antithematic; antiarthritic; antiaesthetic; antibacterial;  
 KW virucide; immunosuppressive; antidiabetic; neuroprotective; muscular;  
 KW dermatological; gene therapy; inflammatory; rheumatoid arthritis; asthma;  
 KW Crohn's disease; allergic hypersensitivity; bacterial; viral infection;  
 KW autoimmune disorder; type I diabetes; multiple sclerosis;  
 KW myasthenia gravis; systemic lupus erythematosus; cancer;  
 KW light chain variable region; human; E55d.





ID ABB74899 standard; protein; 238 AA.  
XX  
AC ABB74899;  
XX  
DT 26-APR-2002 (first entry)  
XX  
DE Humanised anti-Fas antibody light chain SEQ ID NO 131.  
XX  
XX Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;  
KM light chain subunit; apoptosis; immunosuppressive; antiallergic;  
KM autoimmune disease; allergy; atopic.  
XX  
OS Synthetic.  
XX JP2001342148-A.  
XX  
PD 11-DEC-2001.  
XX  
PP 28-MAR-2001; 2001JP-00093106.  
XX  
PR 29-MAR-2000; 2000JP-00090918.  
XX  
XX (SANKYO ) SANKYO CO LTD.  
XX  
DR WPI; 2002-145113/19.  
DR N-PSDB; ABL45939.  
XX  
PT Drug containing humanized anti-Fas antibody, used for preventing and  
PT treating autoimmune diseases, allergy, and atopy.  
XX  
XX Claim 1; Page 133-134; 194pp; Japanese.  
XX  
PS The invention relates to a preventive or treating agent for diseases  
CC caused by abnormality in Fas/Fas ligand system containing as the active  
CC component an antibody having as the light chain subunit a polypeptide  
CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,  
CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all  
CC fully defined in the specification and having an activity of combining  
CC specifically with mammalian Fas and an activity of inducing apoptosis in  
CC a cell expressing Fas. The agent has immunosuppressive and antiallergic  
CC activity and is used for preventing and treating autoimmune diseases,  
CC allergy, atopy and others  
XX  
SQ Sequence 238 AA;  
Query Match 82.3%; Score 489; DB 5; Length 238;  
Best Local Similarity 86.0%; Pred. No. 4.7e-25;  
Matches 98; Conservative 4; Mismatches 12; Indels 0; Gaps 0;  
QY 1 DIGMTQSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNTLS 60  
DB 21 DIVLTQSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNWYQOKPGKAPKLLIYAASNTLS 80  
QY 61 GVPSSRSGSGSGSDFTLTITSSLOPEDPATYCOHSMGIRPTGCGTKVETIKRTV 114  
DB 81 GVPSSRSGSGSGSDFTLTITSSLOPEDPATYCOQSNEDPRTPGCGTKVETIKRTV 134  
RESULT 10  
AAM90932  
ID AAM90932 standard; protein; 238 AA.  
XX  
AC AAM90932;  
XX  
DT 08-AUG-2000 (first entry)  
XX  
DE Humanised anti-Fas designed light chain Leu 3 protein.  
XX  
XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KM anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;  
KM dermatological; immunosuppressive; chylomicemic; antineumatic; anti-Fas;  
KM nephrotoxic; anti-infertility; neuroprotective; antiarteriosclerotic;  
KM hepatocytic; humanized; apoptosis; systemic lupus erythematosus;

KM Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KM Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KM Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KM multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KM insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KM cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX  
OS Synthetic.  
XX EP990663-A2.  
XX  
XX 05-APR-2000.  
XX  
PP 29-SEP-1999; 99EP-00307711.  
XX  
PR 30-SEP-1998; 98JP-00276881.  
PR 30-SEP-1998; 98JP-00276882.  
XX  
XX (SANKYO ) SANKYO CO LTD.  
XX  
XX Serizawa N, Haryuma H, Nakahara K, Tamaki I, Takahashi T;  
DR WPI; 2000-258930/23.  
DR N-PSDB; AAL1633.  
XX  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PT cells with abnormal Fas-Fas ligand systems.  
XX  
XX Claim 3; Page 161-162; 263pp; English.  
XX  
PS This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thymimetic,  
CC antineumatic, nephrotoxic, anti-infertility, neuroprotective,  
CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody light chain construct designated Leu 3  
CC which is described in the method of the invention  
XX  
SQ Sequence 238 AA;  
Query Match 82.2%; Score 488; DB 3; Length 238;  
Best Local Similarity 85.1%; Pred. No. 5.4e-25;  
Matches 97; Conservative 5; Mismatches 12; Indels 0; Gaps 0;  
QY 1 DIGMTQSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNTLS 60  
DB 21 DIVLTQSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNWYQOKPGKAPKLLIYAASNTLS 80  
QY 61 GVPSSRSGSGSGSDFTLTITSSLOPEDPATYCOHSMGIRPTGCGTKVETIKRTV 114  
DB 81 GVPSSRSGSGSGSDFTLTITSSLOPEDPATYCOQSNEDPRTPGCGTKVETIKRTV 134





XX 15-MAY-1997 (first entry)  
 DT Light chain #1 for anti-HB virus antibody.  
 XX  
 DE  
 XX  
 XX  
 KM Antibody; heavy chain; light chain; variable region; human; monoclonal;  
 KM complementarity determining region; human; adr type hepatitis B virus;  
 KM HB virus; CDR; virus antigen; anti-HB antibody; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP09020798-A.  
 XX  
 XX 21-JAN-1997.  
 PD  
 XX 11-JUL-1995; 95JP-00174752.  
 PF  
 XX 11-JUL-1995; 95JP-00174752.  
 PR  
 XX 11-JUL-1995; 95JP-00174752.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 DR WPI; 1997-140911/13.  
 DR N-PSDB; AAT60117.  
 PT Human anti-Hepatitis B antibody - used in a adr type HB virus vaccine.  
 XX  
 PS Claim 7; Page 10-11; 20pp; Japanese.  
 XX  
 CC AAM1921-W1928 represent the sequences for the heavy and light chains of  
 CC the human monoclonal antibodies of the invention. The antibody of the  
 CC invention preferably contains the sequence represented by AAM13912 in the  
 CC complementarity determining region-1 (CDR-1) of the heavy chain variable  
 CC region. The antibody of the invention also contains the sequence  
 CC represented by AAM13913 in the CDR-3 of the light chain variable region.  
 CC The antibody is capable of binding to adr type hepatitis B (HB) virus  
 CC antigen. A human anti-HB virus monoclonal antibody preparation which is  
 CC highly safe and is effective to adr type HB virus can be provided, using  
 CC the monoclonal antibody. It can also be used as a vaccine against HB  
 CC infection  
 XX  
 SO Sequence 114 AA;  
 Query Match 81.8%; Score 486; DB 2; Length 114;  
 Best Local Similarity 84.1%; Pred. No. 4e-25;  
 Matches 95; Conservative 9; Mismatches 5; Indels 4; Gaps 1;  
 QY 2 IOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTESG 61  
 DB 1 LEMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTESG 56  
 QY 62 VPSRFGSGSGGDTFTLTISLQPEDFATYYCOHSMGIPRTFGQGTKEIKRTV 114  
 DB 57 VPSRFGSGSGGDTFTLTISLQPEDFATYYCOHSMGIPRTFGQGTKEIKRTV 109  
 RESULT 14  
 AAM95654  
 ID AAM95654 standard; protein; 114 AA.  
 AC AAM95654;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Mus musculus anti-IgE e426 variable light chain.  
 XX  
 KM Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;  
 KM histamine; production; hypersensitivity; allergen; anaphylaxis;  
 KM atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;  
 KM eczema; anaphylactic shock; urticaria.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO901556-A2.

XX 14-JAN-1999.  
 PD  
 XX 30-JUN-1998; 98WO-US013410.  
 PF  
 XX 02-JUL-1997; 97US-0087352.  
 PR  
 XX (GENTH ) GENENTECH INC.  
 XX  
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;  
 XX  
 DR WPI; 1999-106057/09.  
 XX  
 XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by  
 PT identifying aspartyl residues which undergo isomerization and  
 PT substituting alternative residues and screening for affinity against the  
 PT target.  
 XX  
 PS Disclosure; Page 89-90; 129pp; English.  
 XX  
 CC The sequence is that of the variable light chain of e426. It was used as  
 CC part of a method to improve the affinity of anti-IgE antibodies such as  
 CC e26 and e27. The e26 and e27 antibodies can be used for reducing or  
 CC preventing IgE mediated production of histamine in a mammal. They can be  
 CC used for treating a disorder mediated by IgE such as hypersensitivity,  
 CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,  
 CC eczema, anaphylactic shock and urticaria. The antibodies can also be used  
 CC for affinity purification, detection and diagnosis  
 XX  
 SO Sequence 114 AA;  
 Query Match 81.8%; Score 486; DB 2; Length 114;  
 Best Local Similarity 86.0%; Pred. No. 4e-25;  
 Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 DB 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 QY 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 DB 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 RESULT 15  
 AAM95655  
 ID AAM95655 standard; protein; 114 AA.  
 AC AAM95655;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Mus musculus anti-IgE e25 variable light chain.  
 XX  
 KM Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;  
 KM histamine; production; hypersensitivity; allergen; anaphylaxis;  
 KM atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;  
 KM eczema; anaphylactic shock; urticaria.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO901556-A2.  
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 DT 14-JAN-1999.  
 PD  
 XX 30-JUN-1998; 98WO-US013410.  
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 CC e26 and e27. The e26 and e27 antibodies can be used for reducing or  
 CC preventing IgE mediated production of histamine in a mammal. They can be  
 CC used for treating a disorder mediated by IgE such as hypersensitivity,  
 CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,  
 CC eczema, anaphylactic shock and urticaria. The antibodies can also be used  
 CC for affinity purification, detection and diagnosis  
 XX  
 SO Sequence 114 AA;  
 Query Match 81.8%; Score 486; DB 2; Length 114;  
 Best Local Similarity 86.0%; Pred. No. 4e-25;  
 Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 DB 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 QY 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 DB 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 RESULT 15  
 AAM95655  
 ID AAM95655 standard; protein; 114 AA.  
 AC AAM95655;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Mus musculus anti-IgE e25 variable light chain.  
 XX  
 KM Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;  
 KM histamine; production; hypersensitivity; allergen; anaphylaxis;  
 KM atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;  
 KM eczema; anaphylactic shock; urticaria.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO901556-A2.  
 XX  
 DT 14-JAN-1999.  
 PD  
 XX 30-JUN-1998; 98WO-US013410.  
 PF  
 XX 02-JUL-1997; 97US-0087352.  
 PR  
 XX (GENTH ) GENENTECH INC.  
 XX  
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;  
 XX  
 DR WPI; 1999-106057/09.  
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 XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by  
 PT identifying aspartyl residues which undergo isomerization and  
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 CC part of a method to improve the affinity of anti-IgE antibodies such as  
 CC e26 and e27. The e26 and e27 antibodies can be used for reducing or  
 CC preventing IgE mediated production of histamine in a mammal. They can be  
 CC used for treating a disorder mediated by IgE such as hypersensitivity,  
 CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,  
 CC eczema, anaphylactic shock and urticaria. The antibodies can also be used  
 CC for affinity purification, detection and diagnosis  
 XX  
 SO Sequence 114 AA;  
 Query Match 81.8%; Score 486; DB 2; Length 114;  
 Best Local Similarity 86.0%; Pred. No. 4e-25;  
 Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 DB 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 QY 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 DB 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 RESULT 15  
 AAM95655  
 ID AAM95655 standard; protein; 114 AA.  
 AC AAM95655;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Mus musculus anti-IgE e25 variable light chain.  
 XX  
 KM Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;  
 KM histamine; production; hypersensitivity; allergen; anaphylaxis;  
 KM atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;  
 KM eczema; anaphylactic shock; urticaria.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO901556-A2.  
 XX  
 DT 14-JAN-1999.  
 PD  
 XX 30-JUN-1998; 98WO-US013410.  
 PF  
 XX 02-JUL-1997; 97US-0087352.  
 PR  
 XX (GENTH ) GENENTECH INC.  
 XX  
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;  
 XX  
 DR WPI; 1999-106057/09.  
 XX  
 XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by  
 PT identifying aspartyl residues which undergo isomerization and  
 PT substituting alternative residues and screening for affinity against the  
 PT target.  
 XX  
 PS Disclosure; Page 89-90; 129pp; English.  
 XX  
 CC The sequence is that of the variable light chain of e426. It was used as  
 CC part of a method to improve the affinity of anti-IgE antibodies such as  
 CC e26 and e27. The e26 and e27 antibodies can be used for reducing or  
 CC preventing IgE mediated production of histamine in a mammal. They can be  
 CC used for treating a disorder mediated by IgE such as hypersensitivity,  
 CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,  
 CC eczema, anaphylactic shock and urticaria. The antibodies can also be used  
 CC for affinity purification, detection and diagnosis  
 XX  
 SO Sequence 114 AA;  
 Query Match 81.8%; Score 486; DB 2; Length 114;  
 Best Local Similarity 86.0%; Pred. No. 4e-25;  
 Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 DB 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 QY 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 DB 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 RESULT 15  
 AAM95655  
 ID AAM95655 standard; protein; 114 AA.  
 AC AAM95655;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Mus musculus anti-IgE e25 variable light chain.  
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 KM Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;  
 KM histamine; production; hypersensitivity; allergen; anaphylaxis;  
 KM atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;  
 KM eczema; anaphylactic shock; urticaria.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO901556-A2.  
 XX  
 DT 14-JAN-1999.  
 PD  
 XX 30-JUN-1998; 98WO-US013410.  
 PF  
 XX 02-JUL-1997; 97US-0087352.  
 PR  
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 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;  
 XX  
 DR WPI; 1999-106057/09.  
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 CC preventing IgE mediated production of histamine in a mammal. They can be  
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 CC eczema, anaphylactic shock and urticaria. The antibodies can also be used  
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 Query Match 81.8%; Score 486; DB 2; Length 114;  
 Best Local Similarity 86.0%; Pred. No. 4e-25;  
 Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 DB 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 QY 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 DB 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 RESULT 15  
 AAM95655  
 ID AAM95655 standard; protein; 114 AA.  
 AC AAM95655;  
 XX  
 DT 08-JUN-1999 (first entry)  
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 XX  
 KM Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;  
 KM histamine; production; hypersensitivity; allergen; anaphylaxis;  
 KM atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;  
 KM eczema; anaphylactic shock; urticaria.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO901556-A2.  
 XX  
 DT 14-JAN-1999.  
 PD  
 XX 30-JUN-1998; 98WO-US013410.  
 PF  
 XX 02-JUL-1997; 97US-0087352.  
 PR  
 XX (GENTH ) GENENTECH INC.  
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 CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,  
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 Query Match 81.8%; Score 486; DB 2; Length 114;  
 Best Local Similarity 86.0%; Pred. No. 4e-25;  
 Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 DB 1 DIOMTQSSSLASVGDRTVTTCRASQSVSTSYTMWYQOKRGAAPKVLISYASNTES 60  
 QY 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 DB 61 GVPFRFGSGSGGDTFTLTISLQPEDFATYYCOHSHEDPYTFQGTKEIKRTV 114  
 RESULT 15  
 AAM95655  
 ID AAM95655 standard; protein; 114 AA.  
 AC AAM95655;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Mus musculus anti-IgE e25 variable light chain.  
 XX  
 KM Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;  
 KM histamine; production; hypersensitivity; allergen; anaphylaxis;  
 KM atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;  
 KM eczema; anaphylactic shock; urticaria.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO901556-A2.

DR WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by  
PT identifying aspartyl residues which undergo isomerisation and  
PT substituting alternative residues and screening for affinity against the  
PT target.

XX Disclosure; Page 90; 129p; English.

XX The sequence is that of the variable light chain of e25. It was used as  
CC part of a method to improve the affinity of anti-IgE antibodies such as  
CC e26 and e27. The e26 and e27 antibodies can be used for reducing or  
CC preventing IgE mediated production of histamine in a mammal. They can be  
CC used for treating a disorder mediated by IgE such as hypersensitivity,  
CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,  
CC eczema, anaphylactic shock and urticaria. The antibodies can also be used  
CC for affinity purification, detection and diagnosis

XX Sequence 114 AA;

Query Match 81.8%; Score 486; DB 2; Length 114;

Best Local Similarity 86.0%; Pred. No. 4e-25; Mismatches 13; Indels 0; Gaps 0;

Db 1 DIQWTQSPSLASVGDVRRVTTCRAQSVSTSSYSYMMYQOKPKAPKVLISYASNLDS 60  
1 DIQWTQSPSLASVGDVRRVTTCRAQSVSTSSYSYMMYQOKPKAPKVLISYASNLDS 60  
QY 61 GVPFRFSGSGSGTDTFTLTISLSLOPEDPATYVCOHSMGIPRTFGQGTKEIKRTV 114  
61 GVPFRFSGSGSGTDTFTLTISLSLOPEDPATYVCOHSMGIPRTFGQGTKEIKRTV 114  
Db 61 GVPFRFSGSGSGTDTFTLTISLSLOPEDPATYVCOHSMGIPRTFGQGTKEIKRTV 114

Search completed: December 29, 2004, 19:35:41  
Job time : 120.425 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 19:20:34 ; Search time 23.9742 Seconds  
(without alignments)  
457.521 Million cell updates/sec

Title: US-10-044-896-3

Perfect score: 594  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....SMGIPTFGQTKVEIKRTV 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	81.3	123	2	IG kappa chain - h
2	482	81.1	127	2	IG kappa chain V-J
3	474	79.8	108	2	IG kappa chain V r
4	473	79.6	122	2	IG kappa chain - h
5	462	77.8	108	1	IG kappa chain V-I
6	459	77.3	109	2	IG kappa chain - h
7	458	77.1	108	2	IG kappa chain V r
8	457	76.9	131	2	IG kappa chain V-J
9	455	76.6	109	2	IG kappa chain - h
10	453	76.3	111	2	IG kappa chain V-J
11	451	75.9	129	2	IG kappa chain - h
12	448	75.4	125	2	IG kappa chain V-J
13	447.5	75.3	122	2	IG kappa chain - h
14	447.5	75.3	122	2	IG kappa chain V r
15	446	75.1	129	2	IG kappa chain V r
16	444	74.7	117	2	IG kappa chain V r
17	444	74.6	128	2	IG kappa chain var
18	443	74.4	108	2	IG kappa chain V r
19	442	74.4	117	2	IG kappa chain V-J
20	442	74.4	120	2	IG kappa chain V-J
21	442	74.4	125	2	IG kappa chain - h
22	442	74.4	125	2	IG kappa chain V r
23	442	74.4	129	2	IG kappa chain V r
24	441	74.2	107	2	IG kappa chain V
25	441	74.2	108	1	IG kappa chain V-I
26	440	74.1	108	1	IG kappa chain V-I
27	440	74.1	129	1	IG kappa chain pre
28	439.5	74.0	107	2	IG kappa chain V
29	439	73.9	132	2	IG kappa chain - h

30	438	73.7	108	1	IG kappa chain V-I
31	438	73.7	125	2	IG kappa chain - h
32	438	73.7	132	2	IG kappa chain V r
33	437.5	73.7	125	2	IG kappa chain - h
34	437	73.6	108	1	IG kappa chain V-I
35	437	73.6	108	1	IG kappa chain V-I
36	437	73.6	108	2	IG kappa chain V-J
37	437	73.6	125	2	IG kappa chain V-J
38	436	73.4	129	2	IG kappa chain V r
39	435	73.2	111	1	IG kappa chain V r
40	434	73.1	108	1	IG kappa chain V r
41	434	73.1	109	2	IG kappa chain V r
42	433	72.9	108	1	IG kappa chain V-I
43	433	72.9	126	2	IG kappa chain V-I
44	433	72.9	129	2	IG kappa chain V-J
45	432.5	72.8	124	2	IG kappa chain V-J

## ALIGNMENTS

## RESULT 1

S40331  
IG kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40331  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S403312; MUID:94080891; PMID:8258341  
A:Accession: S40331  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-123 <KLE>  
A:Cross-references: EMBL:X72441; NID:G443350; PIDN:CAAS1109.1; PID:G443351  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:32-106/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 483; DB 2; Length 123;  
Best Local Similarity 85.6%; Pred. No. 1.1e-32;  
Matches 95; Conservative 7; Mismatches 5; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITTCASQSVSTSSSYNHWYQKAPKULISASNTES 60  
DB 17 DIQMTQSPSSLSASVGRVTITTCASQSVSTSSSYNHWYQKAPKULISASNTES 72  
QY 61 GVPKRFSGSGGTFTLTISLTQPEDPATYVCOHSMGIPTFGQTKVEIK 111  
DB 73 GVPKRFSGSGGTFTLTISLTQPEDPATYVCOHSMGIPTFGQTKVEIK 123

## RESULT 2

S40367  
IG kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40367  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S403312; MUID:94080891; PMID:8258341  
A:Accession: S40367  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-127 <KLE>  
A:Cross-references: EMBL:X72477  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:33-107/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 482; DB 2; Length 127;



```
Db      1 ELVMTQSPSSLSASVGDVRVITTCRASQGIS---AYLWVYQKPKAKPLILHSASLSQS 56
      QY      61 GVPKRFSGSGSGTDFTLTITSSLPEDPATYTCQHSWGIPRTFGQGTKEIKRT 113
      Db      57 GVPKRFSGSGSGTDFTLTITSSLPEDPATYTCQHSWGIPRTFGQGTKEIKRT 109

RESULT 7
S44122
Ig kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C/Accession: S44122
R/Hawkins, R.E.; Zhu, D.; Owecke, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
Submitted to the EMBL Data Library, March 1994
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A/Reference number: S44105
A/Accession: S44122
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-108 <HAM>
A/Cross-references: EMBL:Z31390; NID:9472976; PIDN:CAAB3265.1; PID:9940533
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      77.1%; Score 458; DB 2; Length 108;
Best Local Similarity 82.1%; Pred. No. 1e-30;
Matches 92; Conservative 7; Mismatches 9; Indels 4; Gaps 1;

QY      1 DIQMTQSPSSLSASVGDVRVITTCRASQSVSTSSSYMMWYQKPKAKPLISYASNLIS 60
      Db      1 DIQMTQSPSSLSASVGDVRVITTCRASQGIS---SYLWVYQKPKAKPLILHSASLSQS 56
      QY      61 GVPKRFSGSGSGTDFTLTITSSLPEDPATYTCQHSWGIPRTFGQGTKEIKR 112
      Db      57 GVPKRFSGSGSGTDFTLTITSSLPEDPATYTCQHSWGIPRTFGQGTKEIKR 108

RESULT 8
S40352
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40352
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chl genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40352
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-131 <KLE>
A/Cross-references: EMBL:X72462; NID:9441392; PIDN:CAAS1130.1; PID:9441393
C/Superfamily: immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match      76.9%; Score 457; DB 2; Length 131;
Best Local Similarity 79.8%; Pred. No. 1.5e-30;
Matches 91; Conservative 8; Mismatches 11; Indels 4; Gaps 1;

QY      1 DIQMTQSPSSLSASVGDVRVITTCRASQSVSTSSSYMMWYQKPKAKPLISYASNLIS 60
      Db      21 DIQMTQSPSSLSASVGNVITTCRASQGIS---NYLWVYQKPKAKPLILHSASLSQS 76
      QY      61 GVPKRFSGSGSGTDFTLTITSSLPEDPATYTCQHSWGIPRTFGQGTKEIKRTV 114
      Db      77 GVPKRFSGSGSGTDFTLTITSSLPEDPATYTCQHSWGIPRTFGQGTKEIKRTV 130

RESULT 9
```

```
S31981
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31981
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McNachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations a
A/Reference number: S31977
A/Accession: S31981
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: EMBL:Z15077; NID:938493; PIDN:CAA78786.1; PID:938494
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      76.6%; Score 455; DB 2; Length 109;
Best Local Similarity 78.8%; Pred. No. 1.8e-30;
Matches 89; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

QY      1 DIQMTQSPSSLSASVGDVRVITTCRASQSVSTSSSYMMWYQKPKAKPLISYASNLIS 60
      Db      1 ELVMTQSPSSLSASVGDVRVITTCRASQDIS---RYLWVYQKPKAKPLILHSASLSQS 56
      QY      61 GVPKRFSGSGSGTDFTLTITSSLPEDPATYTCQHSWGIPRTFGQGTKEIKRT 113
      Db      57 GVPKRFSGSGSGTDFTLTITSSLPEDPATYTCQHSWGIPRTFGQGTKEIKRT 109

RESULT 10
S09963
Ig kappa chain V-J region (103-7E) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C/Accession: S09963
R/Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A/Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodi
A/Reference number: S09955; MUID:90269328; PMID:2347362
A/Accession: S09963
A/Molecule type: mRNA
A/Residues: 1-111 <REI>
A/Cross-references: UNIPROT:Q920B9; EMBL:X51851
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match      76.3%; Score 453; DB 2; Length 111;
Best Local Similarity 74.8%; Pred. No. 2.7e-30;
Matches 83; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGDVRVITTCRASQSVSTSSSYMMWYQKPKAKPLISYASNLIS 60
      Db      1 DIVITQSPASLAVALGRATISCRASQSVSSGSIYMMWYQKPKAKPLILHSASNLIS 60
      QY      61 GVPKRFSGSGSGTDFTLTITSSLPEDPATYTCQHSWGIPRTFGQGTKEIKR 111
      Db      61 GVPKRFSGSGSGTDFTLTINHPVEEDPATYTCQHSWGIPRTFGQGTKEIKR 111

RESULT 11
S40317
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40317
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chl genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40317
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Db 72 GVPNRFGSGSGTDFTLLISSLQPEDFGYYCQQTHTTPTFGQTKVEIK 122

Search completed: December 29, 2004, 19:36:34  
Job time : 24.9742 secs

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Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 18:57:29 / Search time 127.21 Seconds  
(without alignments)  
515.624 Million cell updates/sec

Title: US-10-044-896-3

Perfect score: 594  
Sequence: 1 DIQWTQSPSSLSASVGRVT.....SMGIPTFGQGTKEIKRTV 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464	78.1	108	2 Q9UL77	P01600 homo sapien
2	462	77.8	108	2 Q9UL77	P01600 homo sapien
3	459	77.3	236	2 Q6GMX8	Q6GMX8 homo sapien
4	456.5	76.9	107	2 Q96SA9	Q96SA9 homo sapien
5	455	76.6	236	2 Q6GMX0	Q6GMX0 homo sapien
6	454	76.4	236	2 Q6GMW1	Q6GMW1 homo sapien
7	444	74.7	236	2 Q6PIH7	Q6PIH7 homo sapien
8	444	74.7	236	2 AAH34141	AAH34141 homo sapi
9	441	74.2	108	1 KVI1E_HUMAN	P01597 homo sapien
10	441	74.2	108	2 Q9UL70	P01597 homo sapien
11	440	74.1	108	1 KVI1N_HUMAN	P01606 homo sapien
12	440	74.1	108	1 KVI1W_HUMAN	P01606 homo sapien
13	440	74.1	236	2 Q723Y4	Q723Y4 homo sapien
14	438	73.7	108	1 KVI1B_HUMAN	P01603 homo sapien
15	437	73.6	108	1 KVI1B_HUMAN	P01594 homo sapien
16	437	73.6	108	1 KVI1B_HUMAN	P04430 homo sapien
17	435	73.2	111	1 KVI3R_MOUSE	P01670 mus musculu
18	434	73.1	108	1 KVI3V_MOUSE	P01674 mus musculu
19	433	72.9	108	1 KVI1G_HUMAN	P01599 homo sapien
20	431.5	72.6	107	2 Q9UL81	Q9UL81 homo sapien
21	431	72.6	236	2 Q6PI75	Q6PI75 homo sapien
22	431	72.6	236	2 AAH29444	AAH29444 homo sapi
23	429	72.2	108	1 KVI1A_HUMAN	P01593 homo sapien
24	428	72.1	108	1 KVI1O_HUMAN	P01607 homo sapien
25	428	72.1	111	2 Q920E9	Q920E9 mus musculu
26	428	72.1	234	2 Q72473	Q72473 homo sapien
27	427	71.9	111	1 KVI3S_MOUSE	P01671 mus musculu
28	427	71.9	236	2 Q6GMX9	Q6GMX9 homo sapien
29	426	71.7	108	1 KVI1P_HUMAN	P01608 homo sapien
30	426	71.7	108	1 KVI1S_HUMAN	P01611 homo sapien
31	426	71.7	108	1 KVI1Y_HUMAN	P016362 homo sapien

32	425	71.5	108	1 KVI1F_HUMAN	P01598 homo sapien
33	425	71.5	108	1 KVI1M_HUMAN	P01605 homo sapien
34	425	71.5	108	2 Q9UL79	Q9UL79 homo sapien
35	422.5	71.1	109	1 KVI1T_HUMAN	P01612 homo sapien
36	421.5	71.0	107	1 KVI1D_HUMAN	P01596 homo sapien
37	421	70.9	108	1 KVI1C_HUMAN	P01595 homo sapien
38	419	70.5	236	2 Q6PIH4	Q6PIH4 homo sapien
39	419	70.5	236	2 AAH34146	AAH34146 homo sapi
40	418	70.4	108	1 KVI1R_HUMAN	P01610 homo sapien
41	417	70.2	111	1 KVI3U_MOUSE	P01672 mus musculu
42	413	69.5	108	1 KVI1I_HUMAN	P01604 homo sapien
43	413	69.5	111	1 KVI3T_MOUSE	P01672 mus musculu
44	411	69.2	240	2 Q6PIJ5	Q6PIJ5 homo sapien
45	411	69.2	240	2 AAH17870	AAH17870 homo sapi

ALIGNMENTS

RESULT 1					
ID	Q9UL77	PRELIMINARY;	PRT;	108 AA.	
AC	Q9UL77;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).				
DE	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
OX	NCBI_Taxid:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE:98271139; PubMed:9614934;				
RA	Yu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,				
RA	Young D.C.;				
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal				
RT	fecus."				
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).				
DR	EMBL; AF035037; AAD56273.1; -.				
DR	PIR; B49047; B49047.				
DR	PIR; S34083; S34083.				
DR	HSSP; P01607; 1BMW.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; Ig; 1.				
DR	PROSITE; PSS0835; IG_LIKE; 1.				
FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE 108 AA; 11738 MW; C06681716CAD16F3 CRC64;				
Query Match 78.1%; Score 464; DB 2; Length 108;					
Best local similarity 82.1%; Pred. No. 1,7e-37;					
Matches 92; Conservative 8; Mismatches 8; Indels 4; Gaps 1;					
Qy	1	DIQWTQSPSSLSASVGRVTITTCRASQSVSTSSYSNMYWYQKKGKAPKVLISYASNLES	60		
Db	1	DIQWTQSPSSLSASVGRVTITTCRASQSVSTSSYSNMYWYQKKGKAPKVLISYASNLES	56		
Qy	61	GVPRFSGSGSGDPTITISLQPEDPATYTCQHSKGIPTFGGTKEIKR	112		
Db	57	GVPRFSGSGSGDPTITISLQPEDPATYTCQHSKGIPTFGGTKEIKR	108		
RESULT 2					
ID	KVI1H_HUMAN	STANDARD;	PRT;	108 AA.	
AC	P01600;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	01-OCT-2004 (Rel. 45, Last annotation update)				

DE Ig kappa chain V-I region Hau.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71032830; PubMed=4097974;  
 RA Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within RT subgroup.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 DR PIR; A01868; KIHUHU.  
 DR PDB; 1F6L; X-ray; L=1-108.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IgV\_1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.  
 FT DOMAIN 89 97 Framework-4.  
 FT DOMAIN 98 107 Complementarity-determining-3.  
 FT DISULFID 23 88 By similarity.  
 FT MONITOR 108 108  
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;  
 Query Match 77.8%; Score 462; DB 1; Length 108;  
 Best Local Similarity 82.1%; Pred. No. 2.7e-37;  
 Matches 92; Conservative 8; Mismatches 8; Indels 4; Gaps 1;  
 QY 1 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSYSMHYQOQKGA PKYLISYASNTLS 60  
 DB 1 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSYSMHYQOQKGA PKYLISYASNTLS 56  
 QY 61 GVSRRFSGSGSGDFTLTISLQPEDPATYCCQHSWGIPTFGQGTVEIKR 112  
 DB 57 GVSRRFSGSGSGDFTLTISLQPEDPATYCCQHSWGIPTFGQGTVEIKR 108  
 RESULT 3  
 ID Q6GKX8 PRELIMINARY; PRT; 236 AA.  
 AC Q6GKX8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=23388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marulita K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman W., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywicki M.I., Skalek U., Smaluk D.B., Schnerch A., Schein J.E.,  
 RA Jones S.J., Maiz M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073764; AAH73764.1; -  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR Pfam; PF00047; Ig\_2.  
 DR SMART; SM00409; Ig\_2.  
 DR SMART; SM00407; Ig1; 2.  
 DR SMART; SM00406; IgV\_1.  
 DR PROSITE; PS50835; Ig\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;  
 Query Match 77.3%; Score 459; DB 2; Length 236;  
 Best Local Similarity 79.8%; Pred. No. 1.3e-36;  
 Matches 91; Conservative 9; Mismatches 10; Indels 4; Gaps 1;  
 QY 1 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSYSMHYQOQKGA PKYLISYASNTLS 60  
 DB 23 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSYSMHYQOQKGA PKYLISYASNTLS 78  
 QY 61 GVSRRFSGSGSGDFTLTISLQPEDPATYCCQHSWGIPTFGQGTVEIKR 114  
 DB 79 GVSRRFSGSGSGDFTLTISLQPEDPATYCCQHSWGIPTFGQGTVEIKR 132  
 RESULT 4  
 ID Q96SA9 PRELIMINARY; PRT; 107 AA.  
 AC Q96SA9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain DE variable region (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98375893; PubMed=9712075;  
 RX Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyclonal monoclonal antibodies from RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin RT antibody V region genes.";  
 RL J. Immunol. 161:2020-2031 (1998).  
 DR EMBL; U96396; AAB68785.1; -  
 DR PIR; B49047; B49047.  
 DR PIR; PH0867; PH0867.  
 DR PIR; S16840; S16840.

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DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; 1BWM.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER
FT TER
FT SEQUENCE 107 AA; 11520 MM; 4BB43B9C5B577F16 CRC64;
SQ SEQUENCE 107 AA; 11520 MM; 4BB43B9C5B577F16 CRC64;

Query Match 76.9%; Score 456.5; DB 2; Length 107;
Best Local Similarity 83.0%; Pred. No. 9.1e-37;
Matches 93; Conservative 7; Mismatches 7; Indels 5; Gaps 2;

Qy 1 DIQWTPSSLSASVGRVITTCRASQSVSTSSYMHVYQKPKVLIYSVSNLES 60
Db 1 DIQWTPSSLSASVGRVITTCRASQSVSTSSYMHVYQKPKVLIYSVSNLES 56
61 GVPSRFGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTPGQGTVEIKRTV 112
57 GVPSRFGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTPGQGTVEIKRTV 107

RESULT 5
ID O6GMX0 PRELIMINARY; PRT; 236 AA.
AC O6GMX0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diachenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Borak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skalela U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MM; 864EA08C7B2BFAF CRC64;
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DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; 1g; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MM; 864EA08C7B2BFAF CRC64;

Query Match 76.6%; Score 455; DB 2; Length 236;
Best Local Similarity 78.1%; Pred. No. 3.1e-36;
Matches 89; Conservative 12; Mismatches 9; Indels 4; Gaps 1;

Qy 1 DIQWTPSSLSASVGRVITTCRASQSVSTSSYMHVYQKPKVLIYSVSNLES 60
Db 23 DIQWTPSSLSASVGRVITTCRASQSVSTSSYMHVYQKPKVLIYSVSNLES 78
61 GVPSRFGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTPGQGTVEIKRTV 114
79 GVPSRFGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTPGQGTVEIKRTV 132

RESULT 6
ID O6GMW1 PRELIMINARY; PRT; 236 AA.
AC O6GMW1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diachenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skalela U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MM; 864EA08C7B2BFAF CRC64;
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DR SMART, SM00407; IGcl, 1.  
DR SMART, SM00406; IGv, 1.  
DR PROSITE; PSS0835; IG\_LIKE, 2.  
DR PROSITE; PSS0290; IG\_MHC; UNKNOWN\_1.  
KM Hypothetical protein.  
SQ SEQUENCE 236 AA; 25751 MW; 5BPEA087AFAC437 CRC64;  
Query Match 76.4%; Score 454; DB 2; Length 236;  
Best Local Similarity 80.5%; Pred. No. 3.9e-36;  
Matches 91; Conservative 6; Mismatches 12; Indels 4; Gaps 1;  
QY 2 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISVANSLESG 61  
DB 24 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISVANSLESG 79  
QY 62 VPSRPSGSGSGTDFLTITSSLOPEDPATYTCQHSWGIPTFGQGTKEIKRTV 114  
DB 80 VPSRPSGSGSGTDFLTITSSLOPEDPATYTCQHSWGIPTFGQGTKEIKRTV 132  
RESULT 7  
06P1H7 PRELIMINARY; PRT; 236 AA.  
ID AC Q6P1H7  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22386257; PubMed=12477932;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,  
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strauberg R.,  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC034141; AAH34141.1; -.  
DR InterPro; IPR003599; IG\_-.  
DR InterPro; IPR007110; IG\_LIKE.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00407; IG; 2.  
DR SMART; SM00407; IGcl, 1.  
DR SMART; SM00406; IGv, 1.  
DR PROSITE; PSS0835; IG\_LIKE, 2.

DR PROSITE; PSS0290; IG\_MHC; UNKNOWN\_1.  
KM Hypothetical protein.  
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;  
Query Match 74.7%; Score 444; DB 2; Length 236;  
Best Local Similarity 78.9%; Pred. No. 3.7e-35;  
Matches 90; Conservative 6; Mismatches 14; Indels 4; Gaps 1;  
QY 1 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISVANSLESG 60  
DB 23 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISVANSLESG 78  
QY 61 GVPSRPSGSGSGTDFLTITSSLOPEDPATYTCQHSWGIPTFGQGTKEIKRTV 114  
DB 79 GVPSRPSGSGSGTDFLTITSSLOPEDPATYTCQHSWGIPTFGQGTKEIKRTV 132  
RESULT 8  
AAH34141 PRELIMINARY; PRT; 236 AA.  
ID AC AAH34141  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22386257; PubMed=12477932;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,  
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strauberg R.,  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC034141; AAH34141.1; -.  
DR InterPro; IPR003599; IG\_-.  
DR InterPro; IPR007110; IG\_LIKE.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00407; IG; 2.  
DR SMART; SM00407; IGcl, 1.  
DR SMART; SM00406; IGv, 1.  
DR PROSITE; PSS0835; IG\_LIKE, 2.



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Query Match          74.1%; Score 440; DB 1; Length 108;
Best Local Similarity 69.6%; Pred. No. 3,7e-35;
Matches 78; Conservative 20; Mismatches 10; Indels 4; Gaps 1;

QY 1 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHMYQOKRGKAPKYLISYASNL60
DB 1 DIQMTGSPSSLSASVGBRVITTCRASQSVSTSSYSYMHMYQOKRGKAPKYLISYASNL60

QY 61 GVSRRFSGSGSGTDFLTITSLQPEDPATYTCQHSNGICPTFGQGTVEIKR 112
DB 57 GVSRRFSGSGSGTDFLTITSLQPEDPATYTCQHSNGICPTFGQGTVEIKR 108

RESULT 12
KVLM HUMAN          STANDARD; PRT; 129 AA.
ID P04431;
AC 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announce/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X00965; CA25477.1; ALT_TERM.
DR PIR; A01883; K1HWK.
DR HSSP; P01607; 1BWM.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003923; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_Like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 1 22
FT DOMAIN 23 129 Ig kappa chain V-I region Walker.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 119 Framework-4.
FT DOMAIN 120 129 Complementarity-determining-3.
FT DISULFID 45 110 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2P9 CRC64;

Query Match          74.1%; Score 440; DB 1; Length 129;
Best Local Similarity 79.3%; Pred. No. 4,6e-35;
Matches 88; Conservative 10; Mismatches 9; Indels 4; Gaps 1;

QY 1 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHMYQOKRGKAPKYLISYASNL60
DB 23 DIQMTGSPSSLSASVGBRVITTCRASQSVSTSSYSYMHMYQOKRGKAPKYLISYASNL60

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QY 61 GVSRRFSGSGSGTDFLTITSLQPEDPATYTCQHSNGICPTFGQGTVEIK 111
DB 79 GVSRRFSGSGSGTDFLTITSLQPEDPATYTCQHSNGICPTFGQGTVEIK 129

RESULT 13
Q723Y4
ID 0723Y4; PRELIMINARY; PRT; 236 AA.
AC 0723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulany S.J.,
RA Bosak S., Mcwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC05332; AA05332.1; -.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match          74.1%; Score 440; DB 2; Length 236;
Best Local Similarity 78.1%; Pred. No. 9,1e-35;
Matches 89; Conservative 8; Mismatches 13; Indels 4; Gaps 1;

QY 1 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHMYQOKRGKAPKYLISYASNL60
DB 23 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHMYQOKRGKAPKYLISYASNL60
QY 61 GVSRRFSGSGSGTDFLTITSLQPEDPATYTCQHSNGICPTFGQGTVEIKR 114
DB 79 GVSRRFSGSGSGTDFLTITSLQPEDPATYTCQHSNGICPTFGQGTVEIKR 132

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RESULT 14
KV1K_HUMAN          STANDARD:      PRT;      108 AA.
ID   KV1K_HUMAN
AC   P01603
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region Ka.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_Taxid=9606;
RN   [1]
RP   MEDLINE=76189985; PubMed=818073;
RA   Shinoda T.;
RT   "Comparative structural studies on the light chains of human
RT   immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL   J. Biochem. 77:1277-1296(1975).
CC   -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01869; KIHUKA.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig_V.
DR   InterPro; IPR003596; Ig_Like.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   immunoglobulin V region.
FT   DOMAIN          1      23      Framework-1.
FT   DOMAIN          24     34      Complementarity-determining-1.
FT   DOMAIN          35     49      Framework-2.
FT   DOMAIN          50     56      Complementarity-determining-2.
FT   DOMAIN          57     88      Framework-3.
FT   DOMAIN          89     97      Framework-4.
FT   DOMAIN          98    107      Complementarity-determining-3.
FT   DISULFID        23     88      By similarity.
FT   NON_TER         108      108
SQ   SEQUENCE      108 AA; 11900 MW; 768839FBED5A2F4B CRC64;

Query Match      73.7%; Score 438; DB 1; Length 108;
Best Local Similarity 73.2%; Pred. No. 5.9e-35;
Matches 82; Conservative 15; Mismatches 11; Indels 4; Gaps 1;

QY   1 DIQMTGSPSSLSASVGRVTITCRASQSVSTSSYSYMHYQOKPKAKPLIYSASNTES 60
DB   1 DIQMTGSPSTLSVSGVGRVTITCRASQTV---LSYLMWYQOKPKAKPLIYASNTLET 56

QY   61 GVPSRFSGSGSGDTFTLTISLQPEDPATYTCOHSMGIPRTFGGTVEIKR 112
DB   57 GVPSRFSGSGSGTFTFTTISVZPBPAFYTCQZYLDPRTFGGTVEIKR 108

RESULT 15
KV1B_HUMAN          STANDARD:      PRT;      108 AA.
ID   KV1B_HUMAN
AC   P01594
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_Taxid=9606;
RN   [1]
RP   MEDLINE=72189444; PubMed=5028201;
RX   Schlecht H., Hillebrunn N.;

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RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlgamer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the Bence-
RT   Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -1- MISCELLANEOUS: The structure of the V region was determined by
CC   molecular replacement methods using the known structure of the V
CC   region of the kappa chain RB1.
CC   -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A91653; KIHUAV.
DR   PDB; 1JVS; X-ray; A=1-107.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig_Like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   immunoglobulin V region.
FT   DOMAIN          1      23      Framework-1.
FT   DOMAIN          24     34      Complementarity-determining-1.
FT   DOMAIN          35     49      Framework-2.
FT   DOMAIN          50     56      Complementarity-determining-2.
FT   DOMAIN          57     88      Framework-3.
FT   DOMAIN          89     97      Complementarity-determining-3.
FT   DISULFID        23     88      By similarity.
FT   STRAND          4      5      10     13     15     16
FT   TURN            15     16     19     25     30     31
FT   STRAND          33     38     40     41     44     49
FT   TURN            44     49     50     52     53     54
FT   STRAND          56     57     60     61     62     67
FT   TURN            62     67     68     69     70     75
FT   STRAND          78     80     82     85     90     97
FT   STRAND          97     98     102    106
FT   NON_TER         108      108
SQ   SEQUENCE      108 AA; 11939 MW; E801187EB6F6B9 CRC64;

Query Match      73.6%; Score 437; DB 1; Length 108;
Best Local Similarity 78.6%; Pred. No. 7.3e-35;
Matches 88; Conservative 6; Mismatches 14; Indels 4; Gaps 1;

QY   1 DIQMTGSPSSLSASVGRVTITCRASQSVSTSSYSYMHYQOKPKAKPLIYSASNTES 60
DB   1 DIQMTGSPSSLSASVGRVTITCRASQDIS---DYLMWYQOKPKAKPLIYASNTLET 56

QY   61 GVPSRFSGSGSGDTFTLTISLQPEDPATYTCOHSMGIPRTFGGTVEIKR 112
DB   57 GVPSRFSGSGSGAFTFTLTISLQPEDPATYTCOOYDYLPTWFGGTVEIKR 108

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Job time : 128.21 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 19:36:01 ; Search time 93.9399 Seconds  
(without alignment)  
436.545 Million cell updates/sec

Title: US-10-044-896-3  
Perfect score: 594  
Sequence: 1 D1MTQSPSSLSASVGRVT.....SWGIPRTGQGTVEIKRTV 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues  
Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/pubppa/PC7\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/2/pubppa/PC7US\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/2/pubppa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/2/pubppa/US09C\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/2/pubppa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	594	100.0	114	14	US-10-044-896-3
2	494	83.2	218	15	US-10-378-567-3
3	490	82.5	218	9	US-09-917-410-2
4	489	82.3	238	14	US-10-216-484-127
5	489	82.3	238	14	US-10-384-933-131
6	488	82.2	238	14	US-10-216-484-131
7	488	82.2	238	14	US-10-384-933-131
8	486	81.8	114	9	US-09-920-171-10
9	486	81.8	114	14	US-10-113-996-10
10	486	81.8	114	17	US-10-791-619-10
11	486	81.8	218	9	US-09-802-077-9
12	486	81.8	218	9	US-09-802-096-9
13	486	81.8	218	9	US-09-920-171-13

ALIGNMENTS

14	486	81.8	218	10	US-09-925-179-9	Sequence 9, Appl1
15	486	81.8	218	14	US-10-113-996-13	Sequence 13, Appl1
16	486	81.8	218	17	US-10-813-483-1	Sequence 1, Appl1
17	486	81.8	218	17	US-10-791-619-13	Sequence 13, Appl1
18	486	81.8	669	17	US-10-764-428-21	Sequence 21, Appl1
19	486	81.8	669	17	US-10-764-428-21	Sequence 21, Appl1
20	485	81.6	238	14	US-10-216-484-129	Sequence 129, App
21	485	81.6	238	14	US-10-384-933-129	Sequence 129, App
22	484	81.5	233	16	US-10-663-244-150	Sequence 150, App
23	483	81.3	108	17	US-10-409-814A-4	Sequence 4, Appl1
24	483	81.3	114	9	US-09-920-171-9	Sequence 9, Appl1
25	483	81.3	114	14	US-10-113-996-9	Sequence 9, Appl1
26	483	81.3	114	17	US-10-791-619-9	Sequence 9, Appl1
27	483	81.3	240	9	US-09-192-854-2	Sequence 2, Appl1
28	483	81.3	240	9	US-09-968-561A-2	Sequence 2, Appl1
29	483	81.3	240	10	US-09-868-744A-2	Sequence 2, Appl1
30	483	81.3	240	11	US-09-868-561A-2	Sequence 2, Appl1
31	483	81.3	240	17	US-10-744-774-1	Sequence 1, Appl1
32	482	81.1	108	17	US-10-744-774-17	Sequence 17, Appl1
33	481	81.0	111	9	US-09-920-171-7	Sequence 7, Appl1
34	481	81.0	111	14	US-10-113-996-7	Sequence 7, Appl1
35	481	81.0	111	17	US-10-791-619-7	Sequence 7, Appl1
36	480.5	80.9	110	9	US-09-025-403A-17	Sequence 17, Appl1
37	480.5	80.9	110	9	US-09-974-052-17	Sequence 17, Appl1
38	480.5	80.9	110	9	US-09-974-051-17	Sequence 17, Appl1
39	480.5	80.9	110	10	US-09-974-498-17	Sequence 17, Appl1
40	480.5	80.9	110	10	US-09-874-516-17	Sequence 17, Appl1
41	478	80.5	114	14	US-10-044-896-1	Sequence 1, Appl1
42	477.5	80.4	110	9	US-09-025-403A-15	Sequence 15, Appl1
43	477.5	80.4	110	9	US-09-974-052-15	Sequence 15, Appl1
44	477.5	80.4	110	9	US-09-974-051-15	Sequence 15, Appl1
45	477.5	80.4	110	10	US-09-974-498-15	Sequence 15, Appl1

RESULT 1  
US-10-044-896-3  
Sequence 3, Application US/10044896  
Publication No. US20030166228A1  
GENERAL INFORMATION:  
APPLICANT: Chantharapai, Anan  
APPLICANT: Kim, Jin K.  
APPLICANT: Stewart, Timothy  
TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES  
FILE REFERENCE: GENENT. 074A  
CURRENT APPLICATION NUMBER: US/10/044,896  
CURRENT FILING DATE: 2002-01-09  
PRIORITY APPLICATION NUMBER: 2001-02-22  
PRIORITY FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: This sequence represents a humanized chimeric antibody comprising human and non-human sequences.  
US-10-044-896-3  
Query Match 100.0%; Score 594; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.8e-40;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 D1MTQSPSSLSASVGRVTITTCRASQSVSTSYSTWMTYQOYRGKAPKTLISASTUES 60  
DB 1 D1MTQSPSSLSASVGRVTITTCRASQSVSTSYSTWMTYQOYRGKAPKTLISASTUES 60  
GVSRFRGSGSGSDFTLTSSLPEDPATYTCQHSNGICPTFGQGTVEIKRTV 114

Db 61 GVPSPSGSGSGTDFLTITSSLOPEDFATYYCOHSGWIGIPRTFGQGTKEIKRTV 114

## RESULT 2

US-10-378-567-3

/ Sequence 3, Application US/10378567  
/ Publication No. US2004006208A1  
/ GENERAL INFORMATION:  
/ APPLICANT: KARPUSAS, MICHAEL  
/ APPLICANT: HSU, YEN-MING  
/ APPLICANT: TAYLOR, FREDERICK R.  
/ APPLICANT: ZHENG, ZHONGLI  
/ TITLE OF INVENTION: CO-CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY 5C8 AND  
/ FILE REFERENCE: A096CON1  
/ CURRENT APPLICATION NUMBER: US/10/378,567  
/ PRIOR FILING DATE: 2003-02-28  
/ PRIOR APPLICATION NUMBER: PCT/US01/27352  
/ PRIOR FILING DATE: 2001-08-31  
/ PRIOR APPLICATION NUMBER: 60/276,452  
/ PRIOR FILING DATE: 2001-03-16  
/ PRIOR APPLICATION NUMBER: 60/229,933  
/ PRIOR FILING DATE: 2000-09-01  
/ NUMBER OF SEQ ID NOS: 3  
/ SOFTWARE: Patent Ver. 2.1  
/ SEQ ID NO 3  
/ LENGTH: 218  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ OTHER INFORMATION: humanized 5c8 light chain amino acid  
US-10-378-567-3

Query Match 83.2%; Score 494; DB 15; Length 218;  
Best Local Similarity 79.8%; Pred. No. 3,7e-32;  
Matches 91; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITTCRASQSVSTSYTMHWYQOKPGKAPKVLISYASNLSS 60

Db 1 DIVLTQSPATLSVSPERRATISCRASQSVSTSYTMHWYQOKPGKAPKVLISYASNLSS 60

QY 61 GVPSPSGSGSGTDFLTITSSLOPEDFATYYCOHSGWIGIPRTFGQGTKEIKRTV 114  
Db 61 GVPSPSGSGSGTDFLTITSSLOPEDFATYYCOHSGWIGIPRTFGQGTKEIKRTV 114

## RESULT 3

US-09-917-410-2

/ Sequence 2, Application US/09917410  
/ Patent No. US20020098183A1  
/ GENERAL INFORMATION:  
/ APPLICANT: MARTIN, Ulrich; HASRLBECK, Anton; SCHUMACHER, Guenther;  
/ APPLICANT: CO, Man S.  
/ TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF  
/ MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR  
/ PREVENTION OF ACUTE ORGAN DAMAGE AFTER  
/ EXTRACORPOREAL BLOOD CIRCULATION  
/ NUMBER OF SEQUENCES: 6  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Felte & Lynch  
/ STREET: 805 Third Avenue  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: U.S.A.  
/ ZIP: 10022  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 3.5" Computer Disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: ASCII, Wordperfect 5.1  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/917,410

/ FILING DATE: 26-Jul-2001  
/ CLASSIFICATION: <Unknown>

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 08/578,953

/ FILING DATE: <Unknown>

/ APPLICATION NUMBER: EP 95 114 969.9

/ FILING DATE: 19-Sep-95

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Hanson, No. US20020098183A1man D.

/ REGISTRATION NUMBER: 30,946

/ REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (212) 688-9200

/ TELEFAX: (212) 838-3884

/ INFORMATION FOR SEQ ID NO: 2:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 218

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 82.5%; Score 490; DB 9; Length 218;  
Best Local Similarity 86.0%; Pred. No. 7.8e-32;  
Matches 98; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITTCRASQSVSTSYTMHWYQOKPGKAPKVLISYASNLSS 60

Db 1 DIVLTQSPATLSVSPERRATISCRASQSVSYDGDSTYTMHWYQOKPGKAPKVLISYASNLSS 60

QY 61 GVPSPSGSGSGTDFLTITSSLOPEDFATYYCOHSGWIGIPRTFGQGTKEIKRTV 114  
Db 61 GVPSPSGSGSGTDFLTITSSLOPEDFATYYCOHSGWIGIPRTFGQGTKEIKRTV 114

## RESULT 4

US-10-216-484-127

/ Sequence 127, Application US/10216484  
/ Publication No. US20030103976A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Setizawa, No. US20030103976A1ufusa  
/ APPLICANT: Haruyama, Hideyuki  
/ APPLICANT: Nakahara, Kaori  
/ APPLICANT: Tamaki, Ikuro  
/ APPLICANT: Takahashi, Tohru  
/ TITLE OF INVENTION: Anti-Fas Antibodies  
/ FILE REFERENCE: 980126CIP/HG  
/ CURRENT APPLICATION NUMBER: US/10/216,484  
/ CURRENT FILING DATE: 2002-08-09  
/ PRIOR APPLICATION NUMBER: US/09/499,662  
/ PRIOR FILING DATE: 2000-02-09  
/ PRIOR APPLICATION NUMBER: US 09/053,583  
/ PRIOR FILING DATE: 1998-04-01  
/ NUMBER OF SEQ ID NOS: 165  
/ SEQ ID NO 127  
/ LENGTH: 238  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Designed light  
/ OTHER INFORMATION: chain of humanized anti-Fas antibody  
US-10-216-484-127

Query Match 82.3%; Score 489; DB 14; Length 238;  
Best Local Similarity 86.0%; Pred. No. 1e-31;  
Matches 98; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITTCRASQSVSTSYTMHWYQOKPGKAPKVLISYASNLSS 60  
Db 21 DIVLTQSPATLSASVGDRTITTCRASQSVSYDGDSTYTMHWYQOKPGKAPKVLISYASNLSS 80



```
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PR
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-10
```

```
Query Match      81.8%; Score 486; DB 9; Length 114;
Best Local Similarity 86.0%; Pred. No. 8.8e-32;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQPSLSASVGDRTVITTCRASQSYSTSSYTMHWYQKPKGAPKVLISYASNLSS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQLTQSPSLASVGDRTVITTCRASQSYDYDGDSTMMWYQKPKGAPKLLIYAASYLESS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GVPSPRSQSGSGTDFLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GVPSPRSQSGSGTDFLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

## RESULT 9

```
US-10-113-996-10
/ Sequence 10, Application US/10113996
/ Publication No. US20030149244A1
/ GENERAL INFORMATION:
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-IGB Antibodies
/ FILE REFERENCE: P1123C3US
/ CURRENT APPLICATION NUMBER: US/10/113,996
/ PRIOR FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ PRIOR APPLICATION NUMBER: US 09/920,171
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PR
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-10
```

```
Query Match      81.8%; Score 486; DB 14; Length 114;
Best Local Similarity 86.0%; Pred. No. 8.8e-32;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQPSLSASVGDRTVITTCRASQSYSTSSYTMHWYQKPKGAPKVLISYASNLSS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQLTQSPSLASVGDRTVITTCRASQSYDYDGDSTMMWYQKPKGAPKLLIYAASYLESS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GVPSPRSQSGSGTDFLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GVPSPRSQSGSGTDFLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

## RESULT 10

```
US-10-791-619-10
/ Sequence 10, Application US/10791619
/ Publication No. US20040259077A1
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-IGB Antibodies and Method of Improving Polypeptides
/ FILE REFERENCE: P1123R1
/ CURRENT APPLICATION NUMBER: US/10/791,619
/ PRIOR FILING DATE: 2004-03-02
/ PRIOR APPLICATION NUMBER: US/09/109,207
```

```
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/051,554
/ PRIOR FILING DATE: 1997-07-03
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PR
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-791-619-10
```

```
Query Match      81.8%; Score 486; DB 17; Length 114;
Best Local Similarity 86.0%; Pred. No. 8.8e-32;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQPSLSASVGDRTVITTCRASQSYSTSSYTMHWYQKPKGAPKVLISYASNLSS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQLTQSPSLASVGDRTVITTCRASQSYDYDGDSTMMWYQKPKGAPKLLIYAASYLESS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GVPSPRSQSGSGTDFLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GVPSPRSQSGSGTDFLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

## RESULT 11

```
US-09-802-077-9
/ Sequence 9, Application US/09802077
/ Patent No. US20010033842A1
/ GENERAL INFORMATION:
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
/ FILE REFERENCE: P0718P2C2US
/ CURRENT APPLICATION NUMBER: US/09/802,077
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: US 08/405,617
/ PRIOR FILING DATE: 1995-03-15
/ PRIOR APPLICATION NUMBER: US 08/185,899
/ PRIOR FILING DATE: 1994-01-26
/ PRIOR APPLICATION NUMBER: PCT/US92/06860
/ PRIOR FILING DATE: 1992-08-14
/ PRIOR APPLICATION NUMBER: US 07/879,495
/ PRIOR FILING DATE: 1992-05-07
/ PRIOR APPLICATION NUMBER: US 07/744,768
/ PRIOR FILING DATE: 1991-08-14
/ NUMBER OF SEQ ID NOS: 64
/ SEQ ID NO 9
/ LENGTH: 218
/ TYPE: PR
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: humanized mae11, version 1, light chain
US-09-802-077-9
```

```
Query Match      81.8%; Score 486; DB 9; Length 218;
Best Local Similarity 86.0%; Pred. No. 1.6e-31;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQPSLSASVGDRTVITTCRASQSYSTSSYTMHWYQKPKGAPKVLISYASNLSS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQLTQSPSLASVGDRTVITTCRASQSYDYDGDSTMMWYQKPKGAPKLLIYAASYLESS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GVPSPRSQSGSGTDFLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GVPSPRSQSGSGTDFLTITSLQPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

## RESULT 12

```
US-09-802-096-9
/ Sequence 9, Application US/09802096
```

```
/ Patent No. US20010038839A1
/ GENERAL INFORMATION:
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
/ FILE REFERENCE: P0718P2C3US
/ CURRENT APPLICATION NUMBER: US/09/802,096
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: US 08/405,617
/ PRIOR FILING DATE: 1995-03-15
/ PRIOR APPLICATION NUMBER: US 08/185,899
/ PRIOR FILING DATE: 1994-01-26
/ PRIOR APPLICATION NUMBER: PCT/US92/06860
/ PRIOR FILING DATE: 1992-08-14
/ PRIOR APPLICATION NUMBER: US 07/879,495
/ PRIOR FILING DATE: 1992-05-07
/ PRIOR APPLICATION NUMBER: US 07/744,768
/ PRIOR FILING DATE: 1991-08-14
/ NUMBER OF SEQ ID NOS: 64
/ SEQ ID NO 9
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: humanized mael1, version 1, light chain
US-09-802-096-9

Query Match      81.8%; Score 486; DB 9; Length 218;
Best Local Similarity 86.0%; Pred. No. 1.6e-31;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Cy 1 DIGNTQSPSSLSASVGRVTTTCRASQSVSTSSYSYHMYQOKRGKAPKVLISYASNLES 60
Db 1 DIGNTQSPSSLSASVGRVTTTCRASQSVSDYDGSYHMYQOKRGKAPKVLISYASNLES 60
61 GVPSRFSGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTFGGTVEIKRTV 114
61 GVPSRFSGSGSGDTFTLTISLQPEDPATYTCQSHEDPYTFGGTVEIKRTV 114

RESULT 13
US-09-920-171-13
/ Sequence 13, Application US/09920171
/ Patent No. US20020054878A1
/ GENERAL INFORMATION:
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-1gE Antibodies (as amended)
/ FILE REFERENCE: P1123C2US
/ CURRENT APPLICATION NUMBER: US/09/920,171
/ CURRENT FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 13
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain sequence derived from MAB11
US-09-920-171-13

Query Match      81.8%; Score 486; DB 9; Length 218;
Best Local Similarity 86.0%; Pred. No. 1.6e-31;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Cy 1 DIGNTQSPSSLSASVGRVTTTCRASQSVSTSSYSYHMYQOKRGKAPKVLISYASNLES 60
Db 1 DIGNTQSPSSLSASVGRVTTTCRASQSVSDYDGSYHMYQOKRGKAPKVLISYASNLES 60
```

```
61 GVPSRFSGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTFGGTVEIKRTV 114
61 GVPSRFSGSGSGDTFTLTISLQPEDPATYTCQSHEDPYTFGGTVEIKRTV 114

RESULT 14
US-09-925-179-9
/ Sequence 9, Application US/09925179
/ Publication No. US20030044858A1
/ GENERAL INFORMATION:
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Anti-1gE Antibodies (as amended)
/ FILE REFERENCE: P0718P2C3US
/ CURRENT APPLICATION NUMBER: US/09/925,179
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 08/466,163
/ PRIOR FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: US 08/405,617
/ PRIOR FILING DATE: 1995-03-15
/ PRIOR APPLICATION NUMBER: US 08/185,899
/ PRIOR FILING DATE: 1994-01-26
/ PRIOR APPLICATION NUMBER: PCT/US92/06860
/ PRIOR FILING DATE: 1992-08-14
/ PRIOR APPLICATION NUMBER: US 07/879,495
/ PRIOR FILING DATE: 1992-05-07
/ PRIOR APPLICATION NUMBER: US 07/744,768
/ PRIOR FILING DATE: 1991-08-14
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 9
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: humanized mael1, version 1, light chain
US-09-925-179-9

Query Match      81.8%; Score 486; DB 10; Length 218;
Best Local Similarity 86.0%; Pred. No. 1.6e-31;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Cy 1 DIGNTQSPSSLSASVGRVTTTCRASQSVSTSSYSYHMYQOKRGKAPKVLISYASNLES 60
Db 1 DIGNTQSPSSLSASVGRVTTTCRASQSVSDYDGSYHMYQOKRGKAPKVLISYASNLES 60
61 GVPSRFSGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTFGGTVEIKRTV 114
61 GVPSRFSGSGSGDTFTLTISLQPEDPATYTCQSHEDPYTFGGTVEIKRTV 114

RESULT 15
US-10-113-996-13
/ Sequence 13, Application US/10113996
/ Publication No. US20030149244A1
/ GENERAL INFORMATION:
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-1gE Antibodies
/ FILE REFERENCE: P1123C3US
/ CURRENT APPLICATION NUMBER: US/10/113,996
/ CURRENT FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ PRIOR APPLICATION NUMBER: US 09/920,171
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 13
/ LENGTH: 218
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-13

```

```

Query Match      81.8%; Score 486; DB 14; Length 218;
Best Local Similarity 86.0%; Pred. No. 1.6e-31;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

```

```

QY 1 DIQMTQSPSSLSASVDGVITTCRASQSVSTSSYIMHWYQQKPKAPKVLISYASNTLS 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSASVDGVITTCRASQSVSTSSYIMHWYQQKPKAPKVLISYASNTLS 60

```

```

QY 61 GVPSPRFGSGSGGTDFLTITISLQPEDPATYVCOHSGIPRTFGQGTKEIKRTV 114
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GVPSPRFGSGSGGTDFLTITISLQPEDPATYVCOHSGIPRTFGQGTKEIKRTV 114

```

```

Search completed: December 29, 2004, 19:52:39
Job time : 94.9399 secs

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 18:57:29 ; Search time 132.79 Seconds  
(without alignments)  
515.624 Million cell updates/sec

Title: US-10-044-896-5

Perfect score: 634

Sequence: 1 EVGLVESGGGVLPQSGSLRL.....ISDFPDYWGQGLTVTSAS 119

Scoring table:

BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

UniProt 02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	447	70.5	470	2	Q6PJ4
2	447	70.5	470	2	AAH18747
3	433.5	68.4	121	2	BAD00525
4	428	67.5	113	2	Q9UL90
5	428	67.5	120	2	BAD00414
6	427.5	67.4	473	2	Q6MZV7
7	427.5	67.4	473	2	CAE45920
8	427	67.4	128	2	BAD00406
9	427	67.4	128	2	BAD00444
10	426	67.2	121	2	Q9UL71
11	426	67.2	122	2	BAD00446
12	425.5	67.1	123	2	BAD00520
13	425.5	67.1	479	2	AAH06402
14	424.5	67.0	613	2	Q6WUX1
15	424	66.9	120	2	BAD00531
16	424	66.9	493	2	Q6GMX2
17	423.5	66.8	119	2	BAD00556
18	423.5	66.8	471	2	AAH24289
19	420.5	66.3	131	2	BAD00439
20	420	66.2	120	2	BAD00465
21	419.5	66.2	483	2	Q6MZK9
22	419.5	66.2	483	2	CAE45898
23	418.5	66.0	121	2	BAD00463
24	418.5	66.0	125	2	BAD00439
25	418	65.9	120	2	BAD00507
26	418	65.9	597	2	Q96B89
27	416.5	65.7	121	2	BAD00404
28	416.5	65.7	606	2	Q6GM72
29	416	65.6	120	2	BAD00488
30	416	65.6	126	2	BAD00529
31	416	65.6	464	2	Q6MZU6

32	416	65.6	464	2	CAE45931	CAE45931 homo sapi
33	415.5	65.5	125	2	BAD00448	BAD00448 camelus d
34	415.5	65.5	127	2	BAD00564	BAD00564 camelus d
35	415.5	65.5	465	2	Q6P6C4	Q6P6C4 homo sapien
36	415.5	65.5	165	2	AAH62335	AAH62335 homo sapi
37	415	65.5	37	2	Q9UL93	Q9UL93 homo sapien
38	415	65.5	122	2	BAD00470	BAD00470 camelus d
39	414.5	65.4	119	2	BAD00471	BAD00471 camelus d
40	414	65.3	117	2	AAH35875	AAH35875 lama glam
41	414	65.3	118	2	BAD00487	BAD00487 camelus d
42	414	65.3	120	2	BAD00493	BAD00493 camelus d
43	414	65.3	120	2	BAD00503	BAD00503 camelus d
44	414	65.3	120	2	BAD00544	BAD00544 camelus d
45	414	65.3	126	2	BAD00566	BAD00566 camelus d

#### ALIGNMENTS

RESULT 1	ID	Q6PJ4	PRELIMINARY;	PRT;	470 AA.
AC	Q6PJ4				
DT	05-JUL-2004	(TREMBLrel. 27, Created)			
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Primary B-Cells;				
RX	MEBLIN=2388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,				
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,				
RA	Krzywinski M.I., Skelton U., Smallie D.B., Scherch A., Schein J.E.,				
RA	Jones S.J., Maiz M.A.,				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences";				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Primary B-Cells;				
RA	Strausberg R.,				
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: BC018747; AAH18747.1; -				
DR	InterPro: IPR003599; IG_				
DR	InterPro: IPR007110; IG_1like.				
DR	InterPro: IPR003597; IG_C1.				
DR	InterPro: IPR003006; IG_MHC.				
DR	InterPro: IPR003596; IG_V.				
DR	Pfam: PF00654; C1-sect; 3.				
DR	Pfam: PF00654; 1g; 4.				
DR	SMART: SM00409; 1g; 2.				
DR	SMART: SM00407; 1g; 3.				
DR	SMART: SM00406; 1g; 1.				
DR	PROSITE: PS50835; 1G_LIKE; 4.				
DR	PROSITE: PS00290; 1G_MHC; UNKNOWN_2.				



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DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 67.5%; Score 428; DB 2; Length 113;
Best Local Similarity 73.5%; Pred. No. 1.7e-37;
Matches 86; Conservative 6; Mismatches 21; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAATGFTTEYIIHWYRQAPGKLEWVASINPDYDITNY 60
D 1 EVQLVESGGGLVQPGGSLRLSCAATGFTTSSYGMHWYRQAPGKLEWVAFTRYDSNKYY 60
DB 61 NQRFKGFITSLDKSKRTAVYIQMNSLRADPTAVYYCAWISDFPDYWGQGLTVYSS 117
DB 61 ADSVKGRTISRDNSKNTLYIQMNSLRADPTAVYYCAKDL---NYWGQGLTVYSS 113

RESULT 5
BAD00414 PRELIMINARY; PRT; 120 AA.
AC BAD00414;
DT 02-MAR-2004 (TRENBLREL. 27, Created)
DT 02-MAR-2004 (TRENBLREL. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLREL. 27, Last annotation update)
DE Immunoglobulin heavy chain VHJD region (Fragment).
GN IGH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SRP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092052; BAD00414.1; -.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 12724 MW; 19D3BE0E07F7949 CRC64;

Query Match 67.5%; Score 428; DB 2; Length 120;
Best Local Similarity 70.3%; Pred. No. 1.8e-37;
Matches 83; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 2 VOLVESGGGLVQPGGSLRLSCATGYTFTYIIHWYRQAPGKLEWVASINPDYDITNY 61
D 2 VOLVESGGGLVQPGGSLRLSCATGYTFTSSYGMHWYRQAPGKLEWVAIPDGKTYNP 61
DB 2 VOLVESGGGLVQPGGSLRLSCATGYTFTSSYGMHWYRQAPGKLEWVAIPDGKTYNP 61

QY 62 QRFKGFITSLDKSKRTAVYIQMNSLRADPTAVYYCAWISDFPDYWGQGLTVYSSAS 119
D 62 DSVKGRFTISRDNSKNTLYIQMNSLRADPTAVYYCATSSNSVDYWGQGLTVYSSAS 119
DB 62 DSVKGRFTISRDNSKNTLYIQMNSLRADPTAVYYCATSSNSVDYWGQGLTVYSSAS 119

RESULT 6
Q6MZV7 PRELIMINARY; PRT; 473 AA.
AC Q6MZV7;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein DKFZP686C11235.
GN Name=DKFZP686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG THE GERMAN HUMAN CDNA CONSORTIUM;
RA Bloeker H., Boecker M., Mewes H.W., Well B., Amid C., Oanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAE45920.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Ig; 3.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476BA4C0BFC447 CRC64;

Query Match 67.4%; Score 427.5; DB 2; Length 473;
Best Local Similarity 65.1%; Pred. No. 9.8e-37;
Matches 82; Conservative 13; Mismatches 24; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYTFTYIIHWYRQAPGKLEWVASINPDYDITNY 60
D 1 EVQLVESGGGLVQPGGSLRLSCAATGFTTSSYGMHWYRQAPGKLEWVAFTRYDSNKYY 79
DB 20 EVQLVESGGGLVQPGGSLRLSCAATGFTTSSYGMHWYRQAPGKLEWVAFTRYDSNKYY 79

QY 61 NQRFKGFITSLDKSKRTAVYIQMNSLRADPTAVYYCAWISDFPDYWGQGLTV 113
D 80 ADSVKGRTISRDNSKNTLYIQMNSLRADPTAVYYCAKDL---NYWGQGLTVYSS 139
DB 80 ADSVKGRTISRDNSKNTLYIQMNSLRADPTAVYYCAKDL---NYWGQGLTVYSS 139

QY 114 TVSSAS 119
DB 140 TVSSAS 145

RESULT 7
CAE45920 PRELIMINARY; PRT; 473 AA.
AC CAE45920;
DT 02-MAR-2004 (TRENBLREL. 27, Created)
DT 02-MAR-2004 (TRENBLREL. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein DKFZP686C11235.
GN DKFZP686C11235.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RA Bloeker H., Boecker M., Mewes H.W., Well B., Amid C., Oanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAE45920.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Ig; 3.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476BA4C0BFC447 CRC64;

Query Match 67.4%; Score 427.5; DB 2; Length 473;
Best Local Similarity 65.1%; Pred. No. 9.8e-37;
Matches 82; Conservative 13; Mismatches 24; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYTFTYIIHWYRQAPGKLEWVASINPDYDITNY 60
D 1 EVQLVESGGGLVQPGGSLRLSCAATGFTTSSYGMHWYRQAPGKLEWVAFTRYDSNKYY 79
DB 20 EVQLVESGGGLVQPGGSLRLSCAATGFTTSSYGMHWYRQAPGKLEWVAFTRYDSNKYY 79

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DT 02-MAR-2004 (Tremblrel. 27, Created)  
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)  
DE Immunoglobulin heavy chain VHJ region (Fragment).  
GN IGH.  
OS Camelus dromedarius (Dromedary) (Arabian camel).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
OX NCBI\_TaxID=9638;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Honda T., Akahori Y., Kurosawa Y.;  
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and  
RT gamma3 in vivo repertoires."  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB092084; BAD00446.1; -.  
FT NON\_TER  
FT 1  
SQ SEQUENCE 122 AA; 13395 MW; 27043ABFC3A4771D CRC64;

Query Match 67.2%; Score 426; DB 2; Length 122;  
Best Local Similarity 67.2%; Pred. No. 3e-37;  
Matches 84; Conservative 10; Mismatches 22; Indels 8; Gaps 2;

QY 1 EVOLVESGGGLVOPGSGRLSCATSGYTFETYYIHVWQAPGKLEWVASINPDYDITNY 60  
DB 1 DVOLVESGGGLVOPGSGRLSCASGFTFSNTYMTWVQAPGKLEWVSGINQDSNTYY 60  
QY 61 NQRFKGRFTISLDKSKRTAYLQNMNLSRAEDPAVYYC-----ASWIDPFYWGQGLTVTV 115  
DB 61 LDSYKGRFTISRDNKNTLYLQNMNLSKEDTALYYCAMPYVAGW---FGYWGQGLTVTV 117

QY 116 SSAS 119  
DB 118 SSES 121

RESULT 12  
BAD00520 PRELIMINARY; PRT; 123 AA.  
ID BAD00520;  
AC BAD00520;  
DT 02-MAR-2004 (Tremblrel. 27, Created)  
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)  
DE Immunoglobulin heavy chain VHJ region (Fragment).  
GN IGH.  
OS Camelus dromedarius (Dromedary) (Arabian camel).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
OX NCBI\_TaxID=9638;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Honda T., Akahori Y., Kurosawa Y.;  
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and  
RT gamma3 in vivo repertoires."  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB092158; BAD00520.1; -.  
FT NON\_TER  
FT 1  
SQ SEQUENCE 123 AA; 13526 MW; E794FBA8EB95C2C3 CRC64;

Query Match 67.1%; Score 425.5; DB 2; Length 123;  
Best Local Similarity 67.2%; Pred. No. 3.4e-37;  
Matches 82; Conservative 14; Mismatches 23; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGRLSCATSGYTFETYYIHVWQAPGKLEWVASINPDYDITNY 60  
DB 1 EVOLVESGGGLVOPGSGRLSCASGFTFSKFMHMTWVQAPGKLEWVSGINPVGINITY 60  
QY 61 NQRFKGRFTISLDKSKRTAYLQNMNLSRAEDPAVYYCASI--SDFPYWGQGLTVTVSS 117

DB 61 ADSVKGRTISRDNKNTLYLQLDLSIKIEDTAMYYCANLPSPGSDYYDYGQGRQTVTVSS 120  
QY 118 AS 119  
DB 121 ES 122

RESULT 13  
AAH06402 PRELIMINARY; PRT; 479 AA.  
ID AAH06402;  
AC AAH06402;  
DT 02-MAR-2004 (Tremblrel. 27, Created)  
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marubina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,  
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Skalska U., Smallus D.E., Scherch A., Schein J.R.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.R.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC006402; AAH06402.1; -.  
KW Hypothetical protein.

KW SEQUENCE 479 AA; 52281 MW; D74E0C89082A9788 CRC64;

Query Match 67.1%; Score 425.5; DB 2; Length 479;  
Best Local Similarity 65.2%; Pred. No. 1.6e-36;  
Matches 86; Conservative 10; Mismatches 23; Indels 13; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGRLSCATSGYTFETYYIHVWQAPGKLEWVASINPDYDITNY 60  
DB 20 EVOLVESGGGLVOPGSGRLSCASGFTFDYAMHMTWVQAPGKLEWVSGISCSNGSISGY 79  
QY 61 NQRFKGRFTISLDKSKRTAYLQNMNLSRAEDPAVYYCASI-----SDFPYWG 107  
DB 80 ADSVKGRTISRDNKNTLYLQNMNLSRAEDTALYYCANKIDILIVVVPAPRSGSLGFDYW 139

QY 108 GQGLTVTVSSAS 119  
DB 140 GQGLTVTVSSAS 151

RESULT 14  
Q8WUK1 PRELIMINARY; PRT; 613 AA.  
ID Q8WUK1;  
AC Q8WUK1;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Altschul S.F., Collins F.S., Wagner L., Shennan C.M., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diacchento L., Marulita K., Farmer A.A., Rubin G.M., Hong L.,  
RA Capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywnicki M.I., Skaleka U., Smallus D.E., Schermer A., Schein J.E.,  
RA Jones S.U., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strauberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC020240; AAH20240.1; -.  
DR PIR; F36005; F36005.  
DR PIR; G36005; G36005.  
DR PIR; PH1642; PH1642.  
DR PIR; PH1643; PH1643.  
DR PIR; PH1645; PH1645.  
DR PIR; PH1646; PH1646.  
DR PIR; PL0098; PL0098.  
DR PIR; PL0120; PL0120.  
DR PIR; S15590; S15590.  
DR PIR; S31116; S31116.  
DR PIR; S31119; S31119.  
DR PIR; S70442; S70442.  
DR HSSP; P01861; IADO.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-sect; 4.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igy; 1.  
DR PROSITE; PS50835; Ig\_LIKE; 5.  
DR PROSITE; PS00290; Ig\_MHC; UNKNOWN 3.  
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 67.0%; Score 424.5; DB 2; Length 613;  
Best Local Similarity 70.5%; Pred. No. 2.8e-36;  
Matches 86; Conservative 8; Mismatches 25; Indels 3; Gaps 2;

QY 1 EVOLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVROAPGKGLRWASINPDYDITNY 60  
DB 20 QVQLVESGGGVQVQGRSLRLSCAASGFTFSYSGMVRQAPFKGLRWAVISYGSNKTY 79  
QY 61 NORFKRFTISLDKSKRTAYIQNNSLRADPTAVYYCA-SWIS--DFPDYWGQGLTVTVSS 117  
DB 80 ADSVKGRFTISRDNKSKLTLYIQNNSLRADPTAVYYCAKDWSEGVETFDIWGGTMVTVSS 139

QY 118 AS 119  
DB 140 GS 141

RESULT 15  
BAD00531  
ID BAD00531 PRELIMINARY; PRT; 120 AA.  
AC BAD00531;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Immunoglobulin heavy chain VHDJ region (Fragment).  
GN IGVH.  
OS Camelus dromedarius (Dromedary) (Arabian camel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
NCBI\_TaxID=9838;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Honda T., Akahori Y., Kurosawa Y.;  
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and  
RT gamma3 in vivo repertoires";  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB092169; BAD00531.1; -.  
FT NON\_TER 1  
FT NON\_TER 1  
FT NON\_TER 120  
SQ SEQUENCE 120 AA; 13277 MW; 8DB4F604E7677FAE CRC64;

Query Match 66.9%; Score 424; DB 2; Length 120;  
Best Local Similarity 68.9%; Pred. No. 4.8e-37;  
Matches 82; Conservative 7; Mismatches 30; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVROAPGKGLRWASINPDYDITNY 60  
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYSGMVRQAPFKGLRWASINPDYDITNY 60  
QY 61 NORFKRFTISLDKSKRTAYIQNNSLRADPTAVYYCA-SWIS--DFPDYWGQGLTVTVSS 119  
DB 61 ADSVKGRFTISRDNKSKLTLYIQNNSLRADPTAVYYCAKDWSEGVETFDIWGGTMVTVSS 139

Search completed: December 29, 2004, 19:31:33  
Job time : 133.79 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 19:20:34 ; Search time 25.0258 Seconds  
(without alignments)  
457.521 Million cell updates/sec

Title: US-10-044-896-5

Perfect score: 634  
Sequence: 1 EVOLVESGGGVDPGGSLRL.....ISDFPDVWGCGTLVTSSAS 119

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	70.3	135	2	IG heavy chain V r
2	442	69.7	119	2	IG heavy chain - h
3	438	69.1	119	2	IG heavy chain V r
4	437	68.9	119	2	IG heavy chain V r
5	436.5	68.8	124	2	IG heavy chain V r
6	436	68.8	121	2	IG heavy chain V r
7	436	68.8	123	2	IG heavy chain - h
8	436	68.8	140	2	IG heavy chain V r
9	435	68.6	119	2	IG heavy chain - h
10	435	68.6	132	2	IG heavy chain V r
11	434.5	68.5	114	2	IG heavy chain V r
12	434.5	68.5	120	2	IG heavy chain V r
13	434	68.5	140	2	IG heavy chain V r
14	433.5	68.4	128	2	IG heavy chain V r
15	433.5	68.4	140	2	IG heavy chain V r
16	433	68.3	125	2	IG heavy chain V r
17	431	68.0	134	2	IG heavy chain V r
18	429	67.7	121	2	IG heavy chain V r
19	428.5	67.6	120	2	IG heavy chain V-D
20	428.5	67.6	137	2	IG heavy chain V r
21	428	67.5	119	2	IG heavy chain V r
22	427.5	67.4	114	2	IG heavy chain V r
23	427.5	67.4	136	2	IG heavy chain V r
24	427	67.4	138	2	IG heavy chain V r
25	425	67.0	140	2	IG heavy chain V r
26	425	67.0	143	2	IG heavy chain V r
27	424.5	67.0	122	2	IG heavy chain V r
28	424	66.9	130	2	IG heavy chain V r
29	423.5	66.8	120	2	IG heavy chain - h

30	422.5	66.6	147	2	IG variable region
31	422	66.6	117	2	IG heavy chain V r
32	422	66.6	134	2	IG heavy chain V r
33	421.5	66.5	114	2	IG heavy chain - h
34	421	66.4	120	2	IG heavy chain V r
35	421	66.4	121	2	IG heavy chain - h
36	420	66.2	121	2	IG heavy chain - h
37	418	65.9	127	2	IG heavy chain - h
38	417.5	65.9	122	2	IG heavy chain V r
39	417	65.8	121	2	IG heavy chain (su
40	417	65.8	160	2	IG heavy chain pre
41	416.5	65.7	118	2	IG heavy chain (su
42	416.5	65.7	122	2	IG heavy chain V r
43	416.5	65.7	141	2	IG heavy chain V r
44	415.5	65.5	122	2	IG V-D region (K
45	415.5	65.5	151	2	IG heavy chain pre

## ALIGNMENTS

## RESULT 1

S31598

IG heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S31598

R/Cislinier, A.M.; Gauchier, L.; Bouill, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31598

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-135 <CU>

A/Cross-references: EMBL:Z14170; NID:G31001; PIDN:CA78539.1; PID:G31002

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/31-114/Domain: immunoglobulin homology <IMM>

Query Match 70.3%, Score 446; DB 2; Length 135;  
Best Local Similarity 74.8%; Pred. No. 2.2e-34;  
Matches 89; Conservative 5; Mismatches 23; Indels 2; Gaps 1;

QY 1 EVOLVESGGGVDPGGSLRLSCATGTYFETIIMWRQAPGKLEWVASINPDYDITNY 60

DB 17 QVQLVESGGGVDPGGSLRLSCAASGTFSSYGMHWROAPKGLEWVAFPRYDGSNRY 76

QY 61 NQRFKGRFTISLDSKSTAYLQNNSLRADPAVYCA--SWISDFPDVWGCGTLVTSS 117

DB 77 ADSVKGRTISRDSKNTLYQNNSLRAEDTAIVYCAKISWEVSFPDVGCGTLVTSS 135

## RESULT 2

S31107

IG heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C/Accession: S31107

R/Raaphorst, F.M.; Timmers, E.; Kentler, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma

A/Title: Restricted utilization of germ-line VH(3) genes and short diverse third comple

A/Reference number: S31104; MUID:92111633; PMID:1730252

A/Accession: S31107

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-119 <RAA>

A/Cross-references: EMBL:X62955

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>



```

Query Match          69.7%; Score 442; DB 2; Length 119;
Best Local Similarity 73.9%; Pred. No. 4.5e-34;
Matches 88; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCATSGYTFTEYIIHWROAPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWROAPGKLEWVASISGSGSTYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NORFKRFTISLDKSKRTAYLQNSLRABDTAVYYCA--WISDFPDYWGQGLTVVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRABDTAVYYCAKDPGASTYFPDYWGQGLTVVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
D36005
Ig heavy chain V region (M43) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: D36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-references: GB:M34024
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match          69.1%; Score 438; DB 2; Length 119;
Best Local Similarity 72.3%; Pred. No. 1.1e-33;
Matches 86; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCATSGYTFTEYIIHWROAPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWROAPGKLEWVASISGSGSTYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NORFKRFTISLDKSKRTAYLQNSLRABDTAVYYCA--WISDFPDYWGQGLTVVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRABDTAVYYCAKKQNDWDFPDWGGGLTVVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
C36005
Ig heavy chain V region (30p1) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C/Accession: C36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-references: GB:M18513
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match          68.9%; Score 437; DB 2; Length 119;
Best Local Similarity 73.3%; Pred. No. 1.3e-33;
Matches 86; Conservative 7; Mismatches 21; Indels 4; Gaps 2;

QY 1 EVOLVESGGGLVPGGSLRLSCATSGYTFTEYIIHWROAPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWROAPGKLEWVASISGSGSTYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NORFKRFTISLDKSKRTAYLQNSLRABDTAVYYCA--ASWISDFPDYWGQGLTVVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRABDTAVYYCAKDPGASG--FDYWGQGLTVVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S20782
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C/Accession: S20782
R/Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A/Description: Analysis of the Igh and Igg rearranged VH repertoire of human cord blood
A/Reference number: S20765
A/Accession: S20782
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-124 <MOR>
A/Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match          68.8%; Score 436.5; DB 2; Length 124;
Best Local Similarity 69.4%; Pred. No. 1.5e-33;
Matches 86; Conservative 10; Mismatches 21; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCATSGYTFTEYIIHWROAPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWROAPGKLEWVASISGSGSTYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NORFKRFTISLDKSKRTAYLQNSLRABDTAVYYCA-----WISDFPDYWGQGLTV 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRABDTAVYYCAKAKRIALFVAVIPHFDPYWGQGLTV 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 114 TVSS 117
    |||||
DB 121 TVSS 124
    |||||

RESULT 6
G36005
Ig heavy chain V region (M74) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C/Accession: G36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: G36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-121 <SCH>
A/Cross-references: UNIPROT:Q8WUK1; GB:M34031
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match          68.8%; Score 436; DB 2; Length 121;
Best Local Similarity 71.9%; Pred. No. 1.6e-33;
Matches 87; Conservative 6; Mismatches 24; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCATSGYTFTEYIIHWROAPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 1 QVQLVESGGGVVQPGGSLRLSCAASGFTSSYAMHWVQAQPGKLEWVAISYDGSNKYY 60  
QY 61 NQRFKGRFTISLDKSKRTAYIQNNSLRAEDTAIVYYCA-----SWISDFPDYWGQGTLYVSS 116  
Db 61 ADSVKGRTISRDNKNTLYIQNNSLRAEDTAIVYYCAKDRKDWGALPDYWGQGTLYVSS 120  
QY 117 S 117  
Db 121 S 121

## RESULT 7

S3114  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S31114  
R:Rapoport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31114  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-123 <RAA>  
A:Cross-references: EMBL:X62963  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 436; DB 2; Length 123;  
Best Local Similarity 69.0%; Pred. No. 1.7e-33;  
Matches 87; Conservative 8; Mismatches 19; Indels 12; Gaps 2;

QY 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFEYIIHWVQAQPGKLEWVAISINPDYDITNY 60  
Db 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSYAMSWVQAQPGKLEWVAISGSGGSTRY 60  
QY 61 NQRFKGRFTISLDKSKRTAYIQNNSLRAEDTAIVYYCA-----SWISDFPDYWGQGT 111  
Db 61 ADSVKGRTISRDNKNTLYIQNNSLRAEDTAIVYYCAKASLYLRLEWL---FDYWGQGT 117  
QY 112 LVTVSS 117  
Db 118 LVTVSS 123

## RESULT 8

S31686  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31686  
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31686  
A:Molecule type: mRNA  
A:Status: preliminary  
A:Residues: 1-140 <CUI>  
A:Cross-references: EMBL:Z14205; NID:930969; PIDN:CA78574.1; PID:930970  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 436; DB 2; Length 140;  
Best Local Similarity 71.9%; Pred. No. 1.9e-33;  
Matches 87; Conservative 9; Mismatches 21; Indels 4; Gaps 1;

QY 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFEYIIHWVQAQPGKLEWVAISINPDYDITNY 60  
Db 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSYAMSWVQAQPGKLEWVAISGSGGSTRY 60

Db 20 EVQLVESGGGVVQPGGSLRLSCAASGFTFSYAMSWVQAQPGKLEWVAISGSGGSTRY 79  
QY 61 NQRFKGRFTISLDKSKRTAYIQNNSLRAEDTAIVYYCA-----SWISDFPDYWGQGTLYVSS 116  
Db 80 SDSVKGRTISRDNKNTLYIQNNSLRAEDTAIVYYCAKCPAPGSPSPDYWGQGTLYVSS 139  
QY 117 S 117  
Db 140 S 140

## RESULT 9

S31108  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S31108  
R:Rapoport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma  
Eur. J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31108  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-119 <RAA>  
A:Cross-references: EMBL:X62956  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 435; DB 2; Length 119;  
Best Local Similarity 72.3%; Pred. No. 2e-33;  
Matches 86; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFEYIIHWVQAQPGKLEWVAISINPDYDITNY 60  
Db 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSYAMSWVQAQPGKLEWVAISGSGGSTRY 60  
QY 61 NQRFKGRFTISLDKSKRTAYIQNNSLRAEDTAIVYYCA-----SWISDFPDYWGQGTLYVSS 117  
Db 61 ADSVKGRTISRDNKNTLYIQNNSLRAEDTAIVYYCAKDRRLTGTFDYWGQGTLYVSS 119

## RESULT 10

S31603  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31603  
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31603  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-132 <CUI>  
A:Cross-references: EMBL:Z14168; NID:930999; PIDN:CA78537.1; PID:931000  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:30-113/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 435; DB 2; Length 132;  
Best Local Similarity 72.6%; Pred. No. 2.2e-33;  
Matches 85; Conservative 8; Mismatches 24; Indels 0; Gaps 0;

QY 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFEYIIHWVQAQPGKLEWVAISINPDYDITNY 60  
Db 16 EVQLVESGGGVVQPGGSLRLSCAASGFTFSYAMSWVQAQPGKLEWVAISYDGSNKYY 75  
QY 61 NQRFKGRFTISLDKSKRTAYIQNNSLRAEDTAIVYYCAKASLYLRLEWL---FDYWGQGTLYVSS 117  
Db 61 NQRFKGRFTISLDKSKRTAYIQNNSLRAEDTAIVYYCAKASLYLRLEWL---FDYWGQGTLYVSS 117



C:Species: Homo sapiens (man)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #ext\_change 09-Jul-2004  
C:Accession: S70442  
R:Contributor, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.  
MOL: Immunol. 29, 1363-1373, 1992  
A:Title: Igm kappa/lambda EBV human B cell clone: an early step of differentiation of fo  
A:Reference number: S70442; MUID:95024508; PMID:138365  
A:Accession: S70442  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-140 <CUI>  
A:Cross-references: UNIPROT:Q8WUK1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:34-117/Domain: immunoglobulin homology <IM4>

Query Match	Score	DB 2	Length	140;
68.4%	433.5			

QY 1 EVQLVESGGGLVQPQSGSLTSCATSTGYTEYLIIHWRAAPGKGEWVASINDPDITNY 60  
:  
Db 20 QVQLVESGGGVQPGSRLTSCASFISNIGHMWRAPKGLEMAFIRDSNKYY 79  
  
QY 61 NORFGFRFTSIDKSRTAYLQMSLRADDTAVYYCA--WISDFDYWGCGTLTVSS 117  
:  
Db 80 ADSVGRRFTSIDNSKNTLYLQMNSTLRADDTAVYCARHIVGATFDWGCGTLTVSS 139

Search completed: December 29, 2004, 19:36:35  
Job time : 26.0258 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using SW model

Run on: December 29, 2004, 19:36:01 ; Search time 98.0601 Seconds  
(without alignments)  
436.545 Million cell updates/sec

Title: US-10-044-896-5  
Perfect score: 634  
Sequence: 1 EVOLVSGGGLVQPGGSLRL.....ISDFDYWGQGLVTVSSAS 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues  
Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Published Applications AA:  
2: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppaa/US05\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppaa/US04\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppaa/US03\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppaa/US02\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppaa/US01\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppaa/US00\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubppaa/US04\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppaa/US03\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppaa/US02\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppaa/US01\_PUBCOMB.pep:\*  
19: /cgn2\_6/ptodata/2/pubppaa/US00\_PUBCOMB.pep:\*  
20: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	634	100.0	119	US-10-044-896-5	Sequence 5, Appl1
2	499.5	78.8	232	US-09-811-384-10	Sequence 10, Appl1
3	499.5	78.8	232	US-10-404-286-10	Sequence 10, Appl1
4	499.5	78.8	241	US-09-940-166A-1	Sequence 1, Appl1
5	499.5	78.8	241	US-10-762-967-1	Sequence 1, Appl1
6	499.5	78.8	300	US-09-940-166A-7	Sequence 7, Appl1
7	499.5	78.8	300	US-10-227-694-2	Sequence 2, Appl1
8	499.5	78.8	300	US-10-762-967-7	Sequence 2, Appl1
9	499.5	78.8	450	US-09-811-384-12	Sequence 12, Appl1
10	499.5	78.8	450	US-10-404-286-12	Sequence 12, Appl1
11	499.5	78.8	469	US-10-835-641-23	Sequence 23, Appl1
12	499.5	77.7	119	US-10-044-896-2	Sequence 2, Appl1
13	492.5	77.7	452	US-10-818-765-4	Sequence 4, Appl1

14	487	76.8	119	US-09-811-123-2	Sequence 2, Appl1
15	487	76.8	119	US-10-268-501-4	Sequence 4, Appl1
16	487	76.8	119	US-10-608-626-4	Sequence 4, Appl1
17	487	76.8	119	US-10-600-152-13	Sequence 13, Appl1
18	487	76.8	119	US-10-619-754-4	Sequence 4, Appl1
19	487	76.8	119	US-10-719-310-4	Sequence 4, Appl1
20	484.5	76.4	122	US-10-818-765-2	Sequence 2, Appl1
21	481	75.9	451	US-10-423-299-4	Sequence 4, Appl1
22	480.5	75.8	122	US-10-835-641-20	Sequence 20, Appl1
23	477.5	75.3	253	US-09-726-258-52	Sequence 52, Appl1
24	477.5	75.3	253	US-09-726-258-55	Sequence 55, Appl1
25	477.5	75.3	256	US-09-726-258-70	Sequence 70, Appl1
26	477.5	75.3	298	US-09-726-258-60	Sequence 60, Appl1
27	477.5	75.3	452	US-09-726-258-71	Sequence 71, Appl1
28	473	74.6	121	US-09-795-798-5	Sequence 5, Appl1
29	470	74.1	121	US-09-795-798-24	Sequence 24, Appl1
30	468.5	73.9	122	US-10-835-641-26	Sequence 26, Appl1
31	463	73.0	225	US-10-364-953-12	Sequence 12, Appl1
32	463	73.0	225	US-10-379-392-171	Sequence 171, App
33	463	73.0	470	US-10-020-786-9	Sequence 9, Appl1
34	463	73.0	470	US-10-227-694-5	Sequence 5, Appl1
35	462	72.9	119	US-10-267-286A-13	Sequence 13, Appl1
36	462	72.9	119	US-10-267-286A-14	Sequence 14, Appl1
37	461.5	72.8	228	US-10-364-953-14	Sequence 14, Appl1
38	461.5	72.8	449	US-10-253-366-2	Sequence 2, Appl1
39	461.5	72.8	449	US-10-316-694-2	Sequence 2, Appl1
40	461.5	72.8	449	US-10-356-974-2	Sequence 2, Appl1
41	461.5	72.8	449	US-10-423-299-2	Sequence 2, Appl1
42	461.5	72.8	449	US-10-659-825-2	Sequence 2, Appl1
43	461.5	72.8	472	US-10-723-003-54	Sequence 54, Appl1
44	461.5	72.8	527	US-10-182-975-25	Sequence 25, Appl1
45	461.5	72.8	628	US-10-723-003-58	Sequence 58, Appl1

ALIGNMENTS

RESULT 1  
US-10-044-896-5  
; Sequence 5, Application US/10044896  
; Publication No. US2003016228A1  
; GENERAL INFORMATION:  
; APPLICANT: Chantharapai, Anan  
; APPLICANT: Kim, Jin K.  
; APPLICANT: Stewart, Timothy  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES  
; FILE REFERENCE: GENENT. 074A  
; CURRENT APPLICATION NUMBER: US/10/044, 896  
; CURRENT FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: 60/270775  
; PRIOR FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: This sequence represents a humanized chimeric antibody comprising human and non-human sequences.  
US-10-044-896-5  
Query Match 100.0%; Score 634; DB 14; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.8e-50;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVOLVSGGGLVQPGGSLRLSCATSGYTFEYIHVWRQAPGKGLWVASINDYITNY 60  
DB 1 EVOLVSGGGLVQPGGSLRLSCATSGYTFEYIHVWRQAPGKGLWVASINDYITNY 60  
QY 61 NOFKRFTSLDKSKRTAYLQNSLRADTVVYCAWSISDFDYWGQGLVTVSSAS 119

Db 61 NORFKRFTISLDKSRKRTAYLQNSLRABDTAVYYCASWISDFYWGQTLTVSSAS 119

## RESULT 2

US-09-811-384-10

; Sequence 10, Application US/09811384  
; Patent No. US20020081294A1

; GENERAL INFORMATION:

; APPLICANT: Bednar, Martin M.

; Thomas, G. Roger

; Gross, Cordell E.

; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/811,384

; FILING DATE: 20-Dec-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/251652

; FILING DATE: 17-FEB-2000

; APPLICATION NUMBER: 08/788800

; FILING DATE: 22-JAN-1997

; APPLICATION NUMBER: 60/093038

; FILING DATE: 23-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: P1729C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5530

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 232 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-811-384-10

Query Match 78.8%; Score 499.5; DB 9; Length 232;

Best Local Similarity 77.0%; Pred. No. 7,3e-38;

Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

Db 1 EVOLVESGGGLVOPGSGSLRLSCATSGYTFETYYIHWVROAPGKLEWVASINPDYDITNY 60

1 EVOLVESGGGLVOPGSGSLRLSCATSGYTFETYYIHWVROAPGKLEWVASINPDYDITNY 60

61 NORFKRFTISLDKSRKRTAYLQNSLRABDTAVYYCASWIS-----DFDYWGQTLV 113

Db 61 NORFKRFTISLDKSRKRTAYLQNSLRABDTAVYYCASWIS-----DFDYWGQTLV 113

61 NORFKRFTISLDKSRKRTAYLQNSLRABDTAVYYCASWIS-----DFDYWGQTLV 113

114 TVSSAS 119

121 TVSSAS 126

Db 121 TVSSAS 126

RESULT 3

US-10-404-286-10

; Sequence 10, Application US/10404286

; Patent No. US20040057951A1

; GENERAL INFORMATION:

; APPLICANT: Blank, Gregory S.

; Narindray, Daljit S.

; Zapata, Gerardo A.

; TITLE OF INVENTION: Protein Recovery

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

APPLICANT: Bednar, Martin M.

Thomas, G. Roger

Gross, Cordell E.

TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/404,286

FILING DATE: 31-Mar-2006

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/811384

FILING DATE: 20-DEC-2000

APPLICATION NUMBER: 09/251652

FILING DATE: 17-FEB-2000

APPLICATION NUMBER: 08/788800

FILING DATE: 22-JAN-1997

APPLICATION NUMBER: 60/093038

FILING DATE: 23-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Evans, David W.

REGISTRATION NUMBER: NONE

REFERENCE/DOCKET NUMBER: P1729C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1739

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 232 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-10-404-286-10

Query Match 78.8%; Score 499.5; DB 15; Length 232;

Best Local Similarity 77.0%; Pred. No. 7,3e-38;

Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

Db 1 EVOLVESGGGLVOPGSGSLRLSCATSGYTFETYYIHWVROAPGKLEWVASINPDYDITNY 60

1 EVOLVESGGGLVOPGSGSLRLSCATSGYTFETYYIHWVROAPGKLEWVASINPDYDITNY 60

61 NORFKRFTISLDKSRKRTAYLQNSLRABDTAVYYCASWIS-----DFDYWGQTLV 113

Db 61 NORFKRFTISLDKSRKRTAYLQNSLRABDTAVYYCASWIS-----DFDYWGQTLV 113

61 NORFKRFTISLDKSRKRTAYLQNSLRABDTAVYYCASWIS-----DFDYWGQTLV 120

114 TVSSAS 119

121 TVSSAS 126

Db 121 TVSSAS 126

RESULT 4

US-09-940-166A-1

; Sequence 1, Application US/09940166A

; Patent No. US20020058324A1

; GENERAL INFORMATION:

; APPLICANT: Blank, Gregory S.

; Narindray, Daljit S.

; Zapata, Gerardo A.

; TITLE OF INVENTION: Protein Recovery

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,166A  
FILING DATE: 27-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/097,309  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-940-166A-1  
Query Match 78.8%; Score 499.5; DB 9; Length 241;  
Best Local Similarity 77.0%; Pred. No. 7.6e-38;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;  
QY 1 EVQLVESGGGLVPGGSLRLSCATSGYTFETYYIMHWROAPGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVPGGSLRLSCATSGYTFETYYIMHWROAPGKLEWVASINPDYDITNY 60  
QY 61 NORFKRFTISLDKSKRTAVLQNMNSLRADTAIVYYCSWIS-----DFPDYGGGTLV 113  
DB 61 NORFKRFTISLDKSKRTAVLQNMNSLRADTAIVYYCSWIS-----DFPDYGGGTLV 120  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126  
RESULT 5  
US-10-762-967-1  
Sequence 1, Application US/10762967  
Publication No. US20040138426A1  
GENERAL INFORMATION:  
APPLICANT: Blank, Gregory S.  
Narindray, Daljit S.  
Zapata, Gerardo A.  
TITLE OF INVENTION: Protein Recovery  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 09/097,309  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-762-967-1

APPLICATION NUMBER: US/10/762,967  
FILING DATE: 21-Jan-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/097,309  
FILING DATE: 12-Jun-1998  
APPLICATION NUMBER: 60/050951  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-762-967-1  
Query Match 78.8%; Score 499.5; DB 16; Length 241;  
Best Local Similarity 77.0%; Pred. No. 7.6e-38;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;  
QY 1 EVQLVESGGGLVPGGSLRLSCATSGYTFETYYIMHWROAPGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVPGGSLRLSCATSGYTFETYYIMHWROAPGKLEWVASINPDYDITNY 60  
QY 61 NORFKRFTISLDKSKRTAVLQNMNSLRADTAIVYYCSWIS-----DFPDYGGGTLV 113  
DB 61 NORFKRFTISLDKSKRTAVLQNMNSLRADTAIVYYCSWIS-----DFPDYGGGTLV 120  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126  
RESULT 6  
US-09-940-166A-7  
Sequence 7, Application US/09940166A  
Patent No. US20020058324A1  
GENERAL INFORMATION:  
APPLICANT: Blank, Gregory S.  
Narindray, Daljit S.  
Zapata, Gerardo A.  
TITLE OF INVENTION: Protein Recovery  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,166A  
FILING DATE: 27-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/097,309  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 300 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-940-166A-7

Query Match      78.8%; Score 499.5; DB 9; Length 300;
Best Local Similarity 77.0%; Pred. No. 9.5e-38;
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDITNY 60
    |||||
DB 24 EVOLVESGGGLVOPGSGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGTSH 83
    |||||

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRADDTAVYYCASWIS-----DFPDYWGQGTLY 113
    |||||
DB 84 NORFKGRFTISVDKSTSTAYMQWNSLRADDTAVYYCARWRGLNYGPDVRYFDVWGQGTLY 143
    |||||

QY 114 TVSSAS 119
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DB 144 TVSSAS 149
    |||||

RESULT 7
US-10-227-694-2
; Sequence 2, Application US/10227694
; Publication No. US2003007739A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura
; APPLICANT: Andersen, Dana
; TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY
; FILE REFERENCE: P1867R1
; CURRENT APPLICATION NUMBER: US/10/227,694
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/315,209
; PRIOR FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-227-694-2

Query Match      78.8%; Score 499.5; DB 14; Length 300;
Best Local Similarity 77.0%; Pred. No. 9.5e-38;
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDITNY 60
    |||||
DB 24 EVOLVESGGGLVOPGSGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGTSH 83
    |||||

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRADDTAVYYCASWIS-----DFPDYWGQGTLY 113
    |||||
DB 84 NORFKGRFTISVDKSTSTAYMQWNSLRADDTAVYYCARWRGLNYGPDVRYFDVWGQGTLY 143
    |||||

QY 114 TVSSAS 119
    |||||
DB 144 TVSSAS 149
    |||||

RESULT 8
US-10-762-967-7
; Sequence 7, Application US/10762967
; Publication No. US20040138426A1
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
```

```
;
; Narindray, Daljit S.
; Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Mapatcin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/762,967
; FILING DATE: 21-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,309
; FILING DATE: 12-Jun-1998
; FILING DATE: 13-JUN-1997
; APPLICATION NUMBER: 60/050951
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 300 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-762-967-7

Query Match      78.8%; Score 499.5; DB 16; Length 300;
Best Local Similarity 77.0%; Pred. No. 9.5e-38;
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDITNY 60
    |||||
DB 24 EVOLVESGGGLVOPGSGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGTSH 83
    |||||

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRADDTAVYYCASWIS-----DFPDYWGQGTLY 113
    |||||
DB 84 NORFKGRFTISVDKSTSTAYMQWNSLRADDTAVYYCARWRGLNYGPDVRYFDVWGQGTLY 143
    |||||

QY 114 TVSSAS 119
    |||||
DB 144 TVSSAS 149
    |||||

RESULT 9
US-09-811-384-12
; Sequence 12, Application US/09811384
; Patent No. US20020081294A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Grose, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
```



ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/811,384  
FILING DATE: 20-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/251652  
FILING DATE: 17-FEB-2000  
APPLICATION NUMBER: 08/788800  
FILING DATE: 22-JAN-1997  
APPLICATION NUMBER: 60/093038  
FILING DATE: 23-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1729C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 450 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-811-384-12

Query Match 78.8%; Score 499.5; DB 9; Length 450;  
Best Local Similarity 77.0%; Pred. No. 1.4e-37;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVLVESGGGLVPGGSLRLSCATSGYTFETIHWVROAPGKGLWVASINPDYDITNY 60  
DB 1 EVLVESGGGLVPGGSLRLSCATSGYTFETIHWVROAPGKGLWVASINPDYDITNY 60  
QY 61 NQRFKGRFTISLDKSKRTAYLVQMNSLRADPTAVYYCAWIS-----DFPDYWGQGLTV 113  
DB 61 NQRFMDFTISVDKSTSTAVYQWNSLRADPTAVYYCAWNRGLNVPDVRFDVWGQGLTV 120  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 10  
US-10-404-286-12  
Sequence 12, Application US/10404286  
Publication No. US20040057951A1  
GENERAL INFORMATION:  
APPLICANT: Bednar, Martin M.  
Thomas, G. Roger  
Gross, Cordell E.  
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/404,286

FILING DATE: 31-Mar-2006  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/811384  
FILING DATE: 20-DEC-2000  
APPLICATION NUMBER: 09/251652  
FILING DATE: 17-FEB-2000  
APPLICATION NUMBER: 08/788800  
FILING DATE: 22-JAN-1997  
APPLICATION NUMBER: 60/093038  
FILING DATE: 23-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, David W.  
REGISTRATION NUMBER: NONE  
REFERENCE/DOCKET NUMBER: P1729C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1739  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 450 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-10-404-286-12

Query Match 78.8%; Score 499.5; DB 15; Length 450;  
Best Local Similarity 77.0%; Pred. No. 1.4e-37;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVLVESGGGLVPGGSLRLSCATSGYTFETIHWVROAPGKGLWVASINPDYDITNY 60  
DB 1 EVLVESGGGLVPGGSLRLSCATSGYTFETIHWVROAPGKGLWVASINPDYDITNY 60  
QY 61 NQRFKGRFTISLDKSKRTAYLVQMNSLRADPTAVYYCAWIS-----DFPDYWGQGLTV 113  
DB 61 NQRFMDFTISVDKSTSTAVYQWNSLRADPTAVYYCAWNRGLNVPDVRFDVWGQGLTV 120  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 11  
US-10-835-641-23  
Sequence 23, Application US/10835641  
Publication No. US20040236078A1  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
Presta, Leonard G.  
TITLE OF INVENTION: Method for Making Humanized Antibodies  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/835,641  
FILING DATE: 30-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/705,398  
FILING DATE: 02-Nov-2000  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993

APPLICATION NUMBER: 07/715272  
 FILING DATE: 14-JUN-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER: 40,378  
 REFERENCE/DOCKET NUMBER: P0709PID2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1994  
 TELEFAX: 650/352-9881  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 469 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
 US-10-835-641-23

Query Match	78.8%	Score 499.5	DB 17	Length 469
Best Local Similarity	77.0%	Pred. No. 1.5e-37		
Matches 97, Conservative	7	Mismatches 15	Indels 7	Gaps 1

[illegible]

```

RESULT 12
US-10-044-896-2
Sequence 2, Application US/10044896
Publication No. US20030166228A1
GENERAL INFORMATION:
APPLICANT: Chuntarapat, Anan
APPLICANT: Kim, Jin K.
APPLICANT: Stewart, Timothy
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
FILE REFERENCE: GENENT. 074A
CURRENT APPLICATION NUMBER: US/10/044,896
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: 60/270775
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 119
TYPE: PRT
ORGANISM: Murine
US-10-044-896-2

```

[illegible]

RESULT 13  
US-10-818-765-4  
; Sequence 4, Application US/10818765

```

Publication No. US20040202658A1
GENERAL INFORMATION:
APPLICANT: Benyunes, Mark C.
TITLE OF INVENTION: THERAPY OF AUTOIMMUNE DISEASE IN A PATIENT WITH AN
TITLE OF INVENTION: INADEQUATE RESPONSE TO A TNF- $\alpha$  INHIBITOR
FILE REFERENCE: P2027R1-US
CURRENT APPLICATION NUMBER: US/10/818,765
CURRENT FILING DATE: 2004-04-06
PRIOR APPLICATION NUMBER: US 60/461,4819
PRIOR FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 452
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: humanized sequence
US-10-818-765-4

```

Query Match	77.7%;	Score 492.5;	DB 17;	Length 452;
Best Local Similarity	76.4%;	Pred. No. 6	3e-37;	
Matches 97; Conservative	6;	Mismatches 13;	Indels 11;	Gaps 2;

QY	1	EVQVLSVGGGGLVQPGGSLRLSCAATGSGTGYFTFYIHAWROAPGKLEWVASINDYDITNNY	60
Db	1	EVQVLSVGGGGLVQPGGSLRLSCAASGTYFTSYNHWARQAQGKLEWVGAIYFQNGDTSY	60
QY	61	NOFKRFRFTISLDKSKRTAVLQWMSLRADPAAVYYCAS-----WISDFPDYMGGTL	112
Db	61	NOFKRFRFTISYDYSKNTLYLQWMSLRADPAAVYYCARVYYYSNSY---YFDWGGGTL	117
QY	113	VTVSSAS	119
Db	118	VTVSSAS	124

```

RESULT 14
US-09-811-123-2
Sequence 2, Application US/09811123
Patent No. US20020001587A1
GENERAL INFORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Slikowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-EBDB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENENT.073A2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,327
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2

```

```

: TYPE: PRT
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: Humanized Antibody Sequence
:
: US-09-811-123-2

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Query Match Similarity	76.8%	Score 487;	DB 9;	Length 119;
Best Local Similarity	78.2%	Pred. No. 5, 1e-37;		
Matches 93; Conservative	11;	Mismatches 13;	Indels 2;	Gaps 1;

QY 1 EVQLVSSGGGLVQPGGSLRLSCAASGYSYETKEYIHVNRAPAGSGLEWMSINPDDITNY 60  
Db 1 EVQLVSSGGGLVQPGGSLRLSCAASGFTTDTYMDVNRAPAGSGLEWADVNPNGSGSY 60  
QY 61 NQRFKGRFTISLDKSRTAIQLMNSLRADDTAVYYCAWMI--SDPDYVGGGTLVTVSS 117

Db 61 NORFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVVYVCANNLGPSFYFDYWGQGLVTVSS 119

## RESULT 15

US-10-268-501-4  
; Sequence 4, Application US/10268501  
; Publication No. US20030086924A1  
; GENERAL INFORMATION:  
; APPLICANT: Sliwowski, Mark X.  
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies  
; FILE REFERENCE: P1467R2P1  
; CURRENT APPLICATION NUMBER: US/10/268,501  
; PRIOR FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 09/602,812  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141,316  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 4  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized VH sequence  
US-10-268-501-4

Query Match 76.8%; Score 487; DB 14; Length 119;  
Best Local Similarity 78.2%; Pred. No. 5.1e-37;

Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYSYTFEYIIMWVQAPQKGLEWVASINPDYDITNY 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCASGFTFTDYMHWQAPQKGLEWVADVNPNSGGSIT 60  
QY 61 NORFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVVYVCANNLGPSFYFDYWGQGLVTVSS 117  
Db 61 NORFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVVYVCANNLGPSFYFDYWGQGLVTVSS 119

Search completed: December 29, 2004, 19:52:40  
Job time : 99.0601 secs

**This Page Blank (uspiv)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 19:21:17 / Search time 28.6009 Seconds  
(without alignments)  
275.930 Million cell updates/sec

Title: US-10-044-896-5  
Perfect score: 634  
Sequence: 1 EVOLVESGGGLVQPGSLRL.....ISDFPDYWGQGTIVTVSSAS 119

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	503.5	79.4	232	2	US-07-934-373C-27
2	503.5	79.4	232	3	US-08-437-642B-27
3	503.5	79.4	232	5	PCT-US93-07832-27
4	499.5	78.8	232	2	US-07-934-373C-29
5	499.5	78.8	232	2	US-08-788-800-10
6	499.5	78.8	232	3	US-08-437-642B-29
7	499.5	78.8	232	5	PCT-US93-07832-29
8	499.5	78.8	235	2	US-07-934-373C-30
9	499.5	78.8	235	5	US-08-437-642B-30
10	499.5	78.8	235	5	PCT-US93-07832-30
11	499.5	78.8	241	3	US-09-097-309-1
12	499.5	78.8	241	3	US-09-097-171A-1
13	499.5	78.8	241	3	US-09-460-587-1
14	499.5	78.8	241	4	US-09-940-166A-1
15	499.5	78.8	300	4	US-09-097-309-7
16	499.5	78.8	300	3	US-09-097-171A-11
17	499.5	78.8	300	3	US-09-422-712B-3
18	499.5	78.8	300	3	US-09-607-756-3
19	499.5	78.8	300	4	US-09-460-587-7
20	499.5	78.8	300	4	US-09-940-166A-7
21	499.5	78.8	450	2	US-08-788-800-12
22	499.5	78.8	469	2	US-07-934-373C-23
23	499.5	78.8	469	3	US-08-437-642B-23
24	499.5	78.8	469	4	US-08-146-206C-23
25	499.5	78.8	469	4	US-09-705-686-23
26	499.5	78.8	469	4	US-09-705-392A-23
27	499.5	78.8	552	5	PCT-US93-07832-23

28	498.5	78.6	232	2	US-07-934-373C-28	Sequence 28, Appl
29	498.5	78.6	232	3	US-08-437-642B-28	Sequence 28, Appl
30	498.5	78.6	232	5	PCT-US93-07832-28	Sequence 28, Appl
31	495.5	78.2	232	2	US-07-934-373C-26	Sequence 26, Appl
32	495.5	78.2	232	3	US-08-437-642B-26	Sequence 26, Appl
33	495.5	78.2	232	5	PCT-US93-07832-26	Sequence 26, Appl
34	494.5	78.0	232	2	US-07-934-373C-38	Sequence 38, Appl
35	494.5	78.0	232	3	US-08-437-642B-38	Sequence 38, Appl
36	494.5	78.0	232	5	PCT-US93-07832-38	Sequence 38, Appl
37	493.5	77.8	232	2	US-07-934-373C-35	Sequence 35, Appl
38	493.5	77.8	232	3	US-08-437-642B-35	Sequence 35, Appl
39	493.5	77.8	232	5	PCT-US93-07832-35	Sequence 35, Appl
40	493.5	77.8	232	3	US-08-437-642B-36	Sequence 36, Appl
41	493.5	77.8	232	5	PCT-US93-07832-36	Sequence 36, Appl
42	493.5	77.8	232	2	US-07-934-373C-33	Sequence 33, Appl
43	492.5	77.7	232	3	US-08-437-642B-33	Sequence 33, Appl
44	492.5	77.7	232	5	PCT-US93-07832-33	Sequence 33, Appl
45	492.5	77.7	232	5	PCT-US93-07832-33	Sequence 33, Appl

## ALIGNMENTS

RESULT 1  
US-07-934-373C-27  
Sequence 27, Application US/07934373C  
Patent No. 5621337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-27  
Query Match 79.4%, Score 503.5, DB 2, Length 232,  
Best Local Similarity 77.8%, Pred. No. 4.4e-42,  
Matches 98, Conservative 6, Mismatches 15, Gaps 1,  
1 EVOLVESGGGLVQPGSLRLSGLTFTETIIHWKQAPGKLEWVASINPDYITNY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCLATSGYTFETYTHMWRQAPGKGLEWVAGINPKNGSTSH 60  
QY 61 NORFKRFTSLDKSKRTAYLQNNSLRAEDTAVYYCAWSIS-----DFPDYWGQSTLV 113  
Db 61 NORFMDRFTLSVDKSKNTLYLQNNSLRAEDTAVYYCAWRGLNYGPDVRYFDVWGQSTLV 120  
QY 114 TVSSAS 119  
Db 121 TVSSAS 126

RESULT 2  
US-08-437-642B-27  
Sequence 27, Application US/08437642B  
Patent No. 6054297  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-437-642B-27

Query Match 79.4%; Score 503.5; DB 3; Length 232;  
Best Local Similarity 77.8%; Pred. No. 4.4e-42;  
Matches 98; Conservative 6; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCLATSGYTFETYTHMWRQAPGKGLEWVAGINPDYDITNY 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCLATSGYTFETYTHMWRQAPGKGLEWVAGINPKNGSTSH 60  
QY 61 NORFKRFTSLDKSKRTAYLQNNSLRAEDTAVYYCAWSIS-----DFPDYWGQSTLV 113

Db 61 NORFMDRFTLSVDKSKNTLYLQNNSLRAEDTAVYYCAWRGLNYGPDVRYFDVWGQSTLV 120  
QY 114 TVSSAS 119  
Db 121 TVSSAS 126

RESULT 3  
PCT-US93-07832-27  
Sequence 27, Application PC/TUS9307832  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX: 415/952-9881  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-07832-27

Query Match 79.4%; Score 503.5; DB 5; Length 232;  
Best Local Similarity 77.8%; Pred. No. 4.4e-42;  
Matches 98; Conservative 6; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCLATSGYTFETYTHMWRQAPGKGLEWVAGINPDYDITNY 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCLATSGYTFETYTHMWRQAPGKGLEWVAGINPKNGSTSH 60  
QY 61 NORFKRFTSLDKSKRTAYLQNNSLRAEDTAVYYCAWSIS-----DFPDYWGQSTLV 113  
Db 61 NORFMDRFTLSVDKSKNTLYLQNNSLRAEDTAVYYCAWRGLNYGPDVRYFDVWGQSTLV 120  
QY 114 TVSSAS 119  
Db 121 TVSSAS 126

RESULT 4  
US-07-934-373C-29

```
Sequence 29, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-29

Query Match      78.8%; Score 499.5; DB 2; Length 232;
Best Local Similarity 77.0%; Pred. No. 1.1e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGCTFTETYYIHVWROAPGKLEWVASINPDYDITNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCATGCTFTETYYIHVWROAPGKLEWVASINPDYDITNY 60
QY 61 NORFQGRFTISLDKSKRTAYLQMNSLRADTVAVYVCASNIS-----DFPDYWGQGLTV 113
DB 61 NORFQGRFTISLDKSKRTAYLQMNSLRADTVAVYVCASNIS-----DFPDYWGQGLTV 120
QY 114 TVSSAS 119
DB 121 TVSSAS 126

RESULT 5
US-08-788-800-10
Sequence 10, Application US/08788800
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell B.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
```

```
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0887x1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-10

Query Match      78.8%; Score 499.5; DB 2; Length 232;
Best Local Similarity 77.0%; Pred. No. 1.1e-41;
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGCTFTETYYIHVWROAPGKLEWVASINPDYDITNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCATGCTFTETYYIHVWROAPGKLEWVASINPDYDITNY 60
QY 61 NORFQGRFTISLDKSKRTAYLQMNSLRADTVAVYVCASNIS-----DFPDYWGQGLTV 113
DB 61 NORFQGRFTISLDKSKRTAYLQMNSLRADTVAVYVCASNIS-----DFPDYWGQGLTV 120
QY 114 TVSSAS 119
DB 121 TVSSAS 126

RESULT 6
US-08-437-642B-29
Sequence 29, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
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PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/146206  
 FILING DATE: 17-NOV-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/05126  
 FILING DATE: 15-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/715272  
 FILING DATE: 14-JUN-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER: 40,378  
 REFERENCE/DOCKET NUMBER: P0709P2C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1994  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 232 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear

Query Match	78.8%	Score 499.5	DB 3	length 232
Best Local Similarity	77.0%	Pred. 1,1e-41		
Matches	97	Conservative	7	Mismatches 15
			Indels	7
			Gaps	1
QY	1	EVOLVESGGGLVOPGSGRLRLSCATSGYFTETEXIIMHVRQAPKGLIEWASINPDYDITNY	60	
Db	1	EVOLVESGGGLVOPGSGRLRLSCATSGYFTETEXIIMHVRQAPKGLIEWAGINPKNGTISH	60	
QY	61	NQREKGRFTISLDNSKRTAIYLOMNSLRABDTIVYICASNIS-----DFPYMGQGLTY	113	
Db	61	NQRFEDRFTISVDKSTSTAYMQMNSLRABDTIVYICARWRGINSYGFVRYFPVWGQGLTY	120	
QY	114	TVSSAS	119	
Db	121	TVSSAS	126	

RESULT 7  
PCT-US93-07832-29  
Sequence 29, Application PC/TUS9307832  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:

```

? NAME:
? REGISTRATION NUMBER:
? REFERENCE/DOCKET NUMBER: 709P2PCT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE:
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 29:
? SEQUENCE CHARACTERISTICS
? LENGTH: 232 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
?
?
? CDT-US93-07832-29

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[illegible]

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1      RESULT 8
2      US-07-934-373C-30
3      Sequence 30, Application US/07934373C
4      Patent No. 5821337
5      GENERAL INFORMATION:
6      APPLICANT: Paul J. Carter
7      APPLICANT: Leonard G. Presta
8      TITLE OF INVENTION: Immunoglobulin Variants
9      NUMBER OF SEQUENCES: 48
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: Genentech, Inc.
12     STREET: 1 DNA Way
13     CITY: South San Francisco
14     STATE: California
15     COUNTRY: USA
16     ZIP: 94080
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: WinPatIn (Genentech)
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/07/934,373C
24     FILING DATE: 21-Aug-1992
25     CLASSIFICATION: 530
26     APPLICATION DATA:
27     APPLICATION NUMBER: PCT/US92/05126
28     FILING DATE: 15-JUN-1992
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: 07/715272
31     FILING DATE: 14-JUN-1991
32     APPLICATION NUMBER: 07/715272
33     ATTORNEY/AGENT INFORMATION:
34     NAME: Lee, Wendy M.
35     REGISTRATION NUMBER: 40,378
36     REFERENCE/DOCKET NUMBER: P0709P2
37     TELECOMMUNICATION INFORMATION:
38     TELEPHONE: 650/225-1994
39     TELEFAX: 650/952-9881
40     INFORMATION FOR SEQ ID NO: 30:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 235 amino acids
43     TYPE: Amino Acid
44

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TOPOLOGY: Linear  
US-07-934-373C-30

Query Match 78.8%; Score 499.5; DB 2; Length 235;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDTNY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDTNY 60

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 120

QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 9

US-08-437-642B-30  
Sequence 30, Application US/08437642B

Patent No. 6054297

GENERAL INFORMATION:

APPLICANT: Paul J. Carter

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/437,642B

FILING DATE: 09-May-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/934373

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/146206

FILING DATE: 17-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0709P2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-437-642B-30

Query Match 78.8%; Score 499.5; DB 3; Length 235;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;

Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDTNY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDTNY 60

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 120

QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 10

PCT-US93-07832-30  
Sequence 30, Application PC/TUS9307832

Patent No. 6054297

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07832

FILING DATE: 19930820

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/934373

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME:

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 709P2PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE:

TELEFAX: 415/952-9881

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US93-07832-30

Query Match 78.8%; Score 499.5; DB 5; Length 235;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDTNY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDTNY 60

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 120

QY 114 TVSSAS 119  
Db 121 TVSSAS 126

## RESULT 11

US-09-097-309-1  
; Sequence 1, Application US/09097309  
; Patent No. 6121428  
; GENERAL INFORMATION:  
; APPLICANT: Blank, Gregory S.  
; APPLICANT: Narindray, Daljit S.  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: Protein Recovery  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/097,309  
; FILING DATE: 12-Jun-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/050951  
; FILING DATE: 13-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schwartz, Timothy R.  
; REGISTRATION NUMBER: 32171  
; REFERENCE/DOCKET NUMBER: P1105R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-7467  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-097-309-1

Query Match 78.8%; Score 499.5; DB 3; Length 241;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVSGGGLVOPGSLRLSCATSGYTFTEYIIHWROAPGKLEWVASINPDYDITNY 60  
Db 1 EVOLVSGGGLVOPGSLRLSCATSGYTFTEYTMHMRQAPGKLEWVAGINPKNGTSH 60  
QY 61 NORFKGRFTISLDKSRRTAYLQMSLRADPTAVYYCASWIS-----DFPDYWGQGLTV 113  
Db 61 NORFKGRFTISLDKSRRTAYLQMSLRADPTAVYYCASWIS-----DFPDYWGQGLTV 120  
QY 114 TVSSAS 119  
Db 121 TVSSAS 126

## RESULT 12

US-09-097-171A-1  
; Sequence 1, Application US/09097171A  
; Patent No. 6171586  
; GENERAL INFORMATION:  
; APPLICANT: Lam, Xanthe M.  
; APPLICANT: Oesewein, James Q.

; APPLICANT: Ongpibatcanakul, Boonsri  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Wang, Sharon X.  
; APPLICANT: Weisburg, Robert P.  
; APPLICANT: Wong, Rita L.  
; TITLE OF INVENTION: Antibody Formulation  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/097,171A  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/874897  
; FILING DATE: 13-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1089R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-097-171A-1

Query Match 78.8%; Score 499.5; DB 3; Length 241;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVSGGGLVOPGSLRLSCATSGYTFTEYIIHWROAPGKLEWVASINPDYDITNY 60  
Db 1 EVOLVSGGGLVOPGSLRLSCATSGYTFTEYTMHMRQAPGKLEWVAGINPKNGTSH 60  
QY 61 NORFKGRFTISLDKSRRTAYLQMSLRADPTAVYYCASWIS-----DFPDYWGQGLTV 113  
Db 61 NORFKGRFTISLDKSRRTAYLQMSLRADPTAVYYCASWIS-----DFPDYWGQGLTV 120  
QY 114 TVSSAS 119  
Db 121 TVSSAS 126

## RESULT 13

US-09-460-587-1  
; Sequence 1, Application US/09460587  
; Patent No. 6322997  
; GENERAL INFORMATION:  
; APPLICANT: Blank, Gregory S.  
; APPLICANT: Narindray, Daljit S.  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: Protein Recovery  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA

ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipactin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/460,587  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/097,309  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-460-587-1

Query Match 78.8%; Score 499.5; DB 3; Length 241;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSSLRLSCATSGYTFEYIIHWVROAPGKLEWVASINPDYDITNY 60  
DB 1 EVOLVESGGGLVOPGSSLRLSCATSGYTFEYIIHWVROAPGKLEWVASINPDYDITNY 60  
QY 61 NORFKGRFTISLDKSKRTAYLQMNLSRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORFKGRFTISLDKSKRTAYLQMNLSRAEDTAVYYCASWIS-----DFPDYWGQGLTV 120  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 14  
US-09-940-166A-1  
Sequence 1, Application US/09940166A  
Patent No. 6716598  
GENERAL INFORMATION:  
APPLICANT: Blank, Gregory S.  
Narindray, Daljit S.  
Zapata, Gerardo A.  
TITLE OF INVENTION: Protein Recovery  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipactin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,166A  
FILING DATE: 27-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/097,309  
FILING DATE: 13-JUN-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-940-166A-1

Query Match 78.8%; Score 499.5; DB 4; Length 241;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSSLRLSCATSGYTFEYIIHWVROAPGKLEWVASINPDYDITNY 60  
DB 1 EVOLVESGGGLVOPGSSLRLSCATSGYTFEYIIHWVROAPGKLEWVASINPDYDITNY 60  
QY 61 NORFKGRFTISLDKSKRTAYLQMNLSRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORFKGRFTISLDKSKRTAYLQMNLSRAEDTAVYYCASWIS-----DFPDYWGQGLTV 120  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 15  
US-09-097-309-7  
Sequence 7, Application US/09097309  
Patent No. 6121428  
GENERAL INFORMATION:  
APPLICANT: Blank, Gregory S.  
Narindray, Daljit S.  
Zapata, Gerardo A.  
TITLE OF INVENTION: Protein Recovery  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipactin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/097,309  
FILING DATE: 12-Jun-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050951  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

US-09-097-309-7

Query Match 78.8%; Score 499.5; DB 3; Length 300;  
 Best Local Similarity 77.0%; Pred. No. 1.5e-41;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY	1	EVQLVDSGGGLVQPGGSLRLSCA	TSGYTFTEYIIHWYRQAPGKGLEWVASINPDYDITNY	60
Db	24	EVQLVDSGGGLVQPGGSLRLSCA	TSGYTFTEYIIHWYRQAPGKGLEWVASINPDYDITNY	83
QY	61	NORFKGRFTISLDKSKRTAYLQMSL	RAEDTAVYYCASWIS-----DFPDYWGQGTIV	113
Db	84	NORFKGRFTISLDKSKRTAYLQMSL	RAEDTAVYYCASWIS-----DFPDYWGQGTIV	143
QY	114	TVSSAS		
Db	144	TVSSAS		

Search completed: December 29, 2004, 19:37:37  
 Job time : 29.6009 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using BW model

Run on: December 29, 2004, 18:59:15 ; Search time 122.575 Seconds  
(without alignments)  
348.266 Million cell updates/sec

Title: US-10-044-896-5

Perfect score: 634  
Sequence: 1 EVQLVESGGGLVOPGGSRLT.....ISDFPDYWGQGLTVSSAS 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_23Sep04:\*

1: geneeqp1980s:\*  
2: geneeqp1990s:\*  
3: geneeqp2000s:\*  
4: geneeqp2001s:\*  
5: geneeqp2002s:\*  
6: geneeqp2003as:\*  
7: geneeqp2003bs:\*  
8: geneeqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	634	100.0	119	5	AAE28150 Humanised
2	499.5	78.8	232	2	AAW34503 Heavy cha
3	499.5	78.8	232	2	AAV08753 Human ant
4	499.5	78.8	232	5	ABG31888 Humanised
5	499.5	78.8	232	8	ADK18341 Amino aci
6	499.5	78.8	241	2	AAW95614 Humanized
7	499.5	78.8	241	4	AAE66776 rhuMab CD
8	499.5	78.8	277	2	AAW30631 Recombina
9	499.5	78.8	300	2	AAW95623 pS1130 ex
10	499.5	78.8	300	2	AAW30635 Recombina
11	499.5	78.8	300	4	AAE66785 Protein e
12	499.5	78.8	300	6	ABP72746 Anti-CD18
13	499.5	78.8	450	2	AAW34505 Heavy cha
14	499.5	78.8	450	2	AAV08755 Human Igg
15	499.5	78.8	450	5	ABG31890 Full leng
16	499.5	78.8	450	8	ADK18343 Amino aci
17	499.5	78.8	537	3	AAE28147 Murine 9F
18	499.5	78.8	537	3	AAE28147 Murine 9F
19	499.5	78.8	537	3	AAE28147 Murine 9F
20	499.5	78.8	537	3	AAE28147 Murine 9F
21	499.5	78.8	537	3	AAE28147 Murine 9F
22	499.5	78.8	537	3	AAE28147 Murine 9F
23	499.5	78.8	537	3	AAE28147 Murine 9F
24	499.5	78.8	537	3	AAE28147 Murine 9F
25	499.5	78.8	537	3	AAE28147 Murine 9F

#### ALIGNMENTS

26	487	76.8	119	8	ADN12053 Variable
27	487	76.8	119	8	ADP43327 Humanised
28	481	75.9	451	8	ADP11670 anti-CD11
29	480.5	75.8	122	2	AAE30772 huCD3v9,
30	477.5	75.3	253	2	AAE29444 Humanised
31	477.5	75.3	253	2	AAE29454 Humanised
32	477.5	75.3	253	3	AAE29457 Humanised
33	477.5	75.3	253	3	AAE29457 Humanised
34	477.5	75.3	253	3	AAE29457 Humanised
35	477.5	75.3	253	3	AAE29457 Humanised
36	477.5	75.3	253	6	ABU13791 Humanised
37	477.5	75.3	253	6	ABU13793 Humanised
38	477.5	75.3	253	6	ABU13793 Humanised
39	477.5	75.3	253	6	ABU13793 Humanised
40	477.5	75.3	253	7	AAE39089 Humanised
41	477.5	75.3	253	7	AAE39086 Humanised
42	477.5	75.3	256	2	AAE63304 Humanised
43	477.5	75.3	256	2	AAE63304 Humanised
44	477.5	75.3	256	3	AAE63304 Humanised
45	477.5	75.3	256	3	AAE63304 Humanised

RESULT 1	AAE28150	AAE28150 standard; protein; 119 AA.
ID	AAE28150	
XX	AAE28150;	
AC	27-DEC-2002	(first entry)
DT	27-DEC-2002	(first entry)
XX	Humanised 9F3 version 13 (V13) heavy chain variable domain.	
DE	Human; interferon alpha; IFNalpha; insulin-dependent diabetes mellitus; autoimmune disease; systemic lupus erythematosus; autoimmune thyroiditis; antibody therapy; immunosuppressive; antiinflammatory; dermatological;	
KW	9F3 monoclonal antibody; heavy chain variable domain.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
PH	Key	Location/Qualifiers
FT	Region	26..35
FT	Region	/note= "Complementarity determining region 1 (CDR1)"
FT	Region	50..66
FT	Region	/note= "Complementarity determining region 2 (CDR2)"
FT	Region	99..106
FT	Region	/note= "Complementarity determining region 3 (CDR3)"
XX	WO200266649-A2.	
XX	29-AUG-2002.	
XX	29-JAN-2002; 2002WO-US002709.	
XX	22-FEB-2001; 2001US-0270775P.	
XX	PR 09-JAN-2002; 2002US-00044896.	
XX	(GETH ) GENENTECH INC.	
XX	Chuntarapai A, Kim JK, Presta LG, Stewart T;	
XX	WPI; 2002-682767/73.	
XX	New anti-interferon alpha monoclonal antibody, 9F3, useful for treating autoimmune diseases e.g. insulin-dependent diabetes mellitus, systemic lupus erythematosus and autoimmune thyroiditis.	
XX	Disclosure; Page 98; 100p; English.	
XX	The present invention relates to novel anti-interferon alpha (IFNalpha)	

CC monoclonal antibody, 9F3 which binds to and neutralises a biological  
CC activity of IFN-alpha subtypes. The anti-IFNalpha monoclonal antibodies  
CC of the invention are useful for treating autoimmune diseases such as  
CC insulin-dependent diabetes mellitus, systemic lupus erythematosus and  
CC autoimmune thyroiditis. They are useful as reagents in diagnostic assays  
CC for IFN-alpha expression, for the affinity purification of various IFN-  
CC alpha subtypes from recombinant cell culture or natural resources and for  
CC the detection of IFN-alpha in diagnostic assay methods. Sequences of the  
CC invention are also useful in antibody therapy. The present sequence is  
CC anti-human IFNalpha monoclonal antibody 9F3 version 13 (V13) heavy chain  
CC variable domain  
CC  
XX  
SQ Sequence 119 AA;  
  
Query Match 100.0%; Score 634; DB 5; Length 119;  
Best Local Similarity 100.0%; Pred. NO. 4.1e-52;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYIHWRQAPGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYIHWRQAPGKLEWVASINPDYDITNY 60  
  
QY 61 NORFKGFTTSLDKSKRTAYLQNMNLSRAEDTAVYYCASNISDFPDYWGQGLTVVSSAS 119  
DB 61 NORFKGFTTSLDKSKRTAYLQNMNLSRAEDTAVYYCASNISDFPDYWGQGLTVVSSAS 119  
  
RESULT 2  
AAW34503  
ID AAW34503 standard; protein; 232 AA.  
XX  
AC AAW34503;  
XX  
DT 19-MAR-1998 (first entry)  
XX  
DE Heavy chain of humanised H52 antibody.  
XX  
KW Humanised antibody; HuH52; heavy chain; focal ischaemic stroke; embolism;  
KW brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;  
KW transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;  
KW systemic hypoperfusion; cardiac arrest.  
XX  
OS Synthetic.  
OS Homo sapiens.  
OS Mus sp.  
XX  
FN W09726912-A2.  
XX  
PD 31-JUL-1997.  
XX  
PF 11-JAN-1997; 97WO-US000492.  
XX  
PR 23-JAN-1996; 96US-00589982.  
XX  
PA (GETH ) GENENTECH INC.  
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
XX  
PI Bednar MM, Gross CE, Thomas GR;  
XX  
DR WPI; 1997-393373/36.  
XX  
PT Administering an anti-CD18 antibody to treat focal ischaemic stroke - by  
PT increasing cerebral blood flow and reducing size of brain infarct.  
XX  
PS Disclosure; Page 9; 41pp; English.  
XX  
CC This sequence represents the heavy chain of the humanised H52 antibody.  
CC The H52 antibody can be used in the method of the invention. The method  
CC is for treating focal ischaemic stroke, i.e. damage to the brain due to  
CC interrupted blood supply, in a mammal, caused by obstruction of a main  
CC cerebral artery, comprises administering anti-CD18 antibody to increase  
CC cerebral blood flow and/or reduce the size of the area of brain that  
CC dies, without removing the arterial obstruction. CD18, is upregulated in

CC patients after ischaemic stroke or transient ischaemic attack (stroke  
CC symptoms last less than 24 hours with complete recovery). Treatment with  
CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain  
CC infarct size, improving clinical outcomes in focal ischaemic strokes in  
CC mammals, particularly in humans. The method provides an alternative to  
CC thrombolytic therapy for treating ischaemic strokes caused by  
CC thromboembolism (thrombosis or embolism), particularly where thrombolytic  
CC therapy has been unsuccessful, is contra-indicated e.g. because such  
CC drugs exacerbate bleeding, or is unsuitable because of the time delay  
CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue  
CC plasminogen activator) may also be administered before, after or  
CC simultaneously with the anti-CD18 antibody. Alternatively, the method can  
CC be used to treat the third main type of ischaemic stroke, systemic  
CC hypoperfusion, e.g. resulting from cardiac arrest or drowning  
XX  
SQ Sequence 232 AA;  
  
Query Match 78.8%; Score 499.5; DB 2; Length 232;  
Best Local Similarity 77.0%; Pred. No. 4.2e-39;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;  
  
QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYIHWRQAPGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYHWRQAPGKLEWVASINPDYDITNY 60  
  
QY 61 NORFKGFTTSLDKSKRTAYLQNMNLSRAEDTAVYYCASNISDFPDYWGQGLTV 113  
DB 61 NORFKGFTTSLDKSKRTAYLQNMNLSRAEDTAVYYCASNISDFPDYWGQGLTV 120  
  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126  
  
RESULT 3  
AAV08753  
ID AAV08753 standard; protein; 232 AA.  
XX  
AC AAV08753;  
XX  
DT 10-AUG-1999 (first entry)  
XX  
DE Human antibody huH52 heavy chain protein fragment.  
XX  
KW IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;  
KW IgG4; kappa-CU domain; lambda-CU domain; focal ischaemic stroke;  
KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;  
KW CD18 extracellular domain; endothelium; CD1b/CD18 complex dissociation;  
KW antibody; huH52; heavy chain.  
XX  
OS Homo sapiens.  
XX  
FN US5914112-A.  
XX  
PD 22-JUN-1999.  
XX  
PF 22-JAN-1997; 97US-00788800.  
XX  
PR 23-JAN-1996; 96US-0093038P.  
XX  
PA (GETH ) GENENTECH INC.  
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
XX  
PI Thomas GR, Bednar MM, Gross CE;  
XX  
DR WPI; 1999-370483/31.  
XX  
PT Anti-CD18 antibodies in stroke.  
XX  
PS Claim 11; Col 29-32; 25pp; English.  
XX  
CC This invention describes a method for improving the clinical outcome in  
CC focal ischaemic stroke by administering novel anti-CD18 antibody which

CC has cerebroprotective properties. The invention particularly describes a  
CC method of treating focal ischaemic stroke caused by the obstruction of a  
CC main cerebral artery which comprises administering an anti-CD18 antibody  
CC to increase the blood flow or reduce the infarct size, where: (1) the  
CC antibody binds to an extracellular domain of CD18 and inhibits or reduces  
CC the ability of the cell expressing CD18 to bind to endothelium, (2) the  
CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the  
CC antibody dissociates CD18/CD18 complex. This sequence represents the  
CC human antibody huH52 heavy chain region  
XX  
SQ Sequence 232 AA;  
Query Match 78.8%; Score 499.5; DB 2; Length 232;  
Best Local Similarity 77.0%; Pred. No. 4.2e-39;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;  
QY 1 EVQLVESGGGLVPGGSLRLSCLATSGYTFTEYIIHWROAPRGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVPGGSLRLSCLATSGYTFTEYIIHWROAPRGKLEWVASINPDYDITNY 60  
QY 61 NORPKGRFTISLDKSKRTAYLQNNSLRAEDTAAYVYTCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORPKGRFTISLDKSKRTAYLQNNSLRAEDTAAYVYTCASWIS-----DFPDYWGQGLTV 113  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126  
Db 121 TVSSAS 126  
RESULT 4  
ABG31888  
ID ABG31888 standard; peptide; 232 AA.  
XX  
AC ABG31888;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Humanised H52 antibody (huH52) Fab fragment, heavy chain.  
XX  
KW Human; humanised H52 antibody; huH52; cerebral blood flow; infarct size;  
KW focal ischaemic stroke; main cerebral artery;  
KW tissue plasminogen activator; anti-CD18 antibody; stroke;  
KW acute ischaemic stroke; thrombolytic therapy;  
KW Fab/ab salvage receptor binding epitope; thromboembolic stroke.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN US2002081294-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 20-DEC-2000; 2000US-00811384.  
XX  
PR 23-JAN-1996; 96US-0093038P.  
PR 22-JAN-1997; 97US-00788800.  
PR 17-FEB-1999; 99US-00251652.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Bednar MM, Gross CE, Thomas GR, Gross LJ;  
XX  
DR WPI; 2004-626528/67.  
XX  
PT Increasing cerebral blood flow and/or reducing infarct size in focal  
PT ischemic stroke using anti-CD18 antibody and tissue plasminogen activator  
PT is useful to improve clinical outcome in acute ischemic stroke.  
XX  
PS Claim 11; Page 5; 27pp; English.  
XX  
CC The invention relates to a method of increasing cerebral blood flow and/  
CC or reducing infarct size in focal ischaemic stroke caused by obstruction  
CC of a main cerebral artery in a human, comprising co-administering tissue

CC plasminogen activator and anti-CD18 antibody about 3-5 hours after the  
CC stroke. The method is used to improve the clinical outcome in acute  
CC ischaemic stroke and to provide an alternative to thrombolytic therapy  
CC for treating thromboembolic stroke, particularly where thrombolytic  
CC therapy has been unsuccessful or is contra-indicated. The present  
CC sequence represents a humanised H52 antibody (huH52) Fab, heavy chain  
CC used in the method of the invention  
XX  
SQ Sequence 232 AA;  
Query Match 78.8%; Score 499.5; DB 5; Length 232;  
Best Local Similarity 77.0%; Pred. No. 4.2e-39;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;  
QY 1 EVQLVESGGGLVPGGSLRLSCLATSGYTFTEYIIHWROAPRGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVPGGSLRLSCLATSGYTFTEYIIHWROAPRGKLEWVASINPDYDITNY 60  
QY 61 NORPKGRFTISLDKSKRTAYLQNNSLRAEDTAAYVYTCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORPKGRFTISLDKSKRTAYLQNNSLRAEDTAAYVYTCASWIS-----DFPDYWGQGLTV 113  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126  
Db 121 TVSSAS 126  
RESULT 5  
ADK18341  
ID ADK18341 standard; protein; 232 AA.  
XX  
AC ADK18341;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Amino acid sequence of humanised H52 (huH52) Fab heavy chain.  
XX  
KW Cerebral blood flow; infarct size; focal ischaemic stroke;  
KW cerebral artery; tissue plasminogen activator; tPA; anti-CD18 antibody;  
KW humanised H52 antibody; huH52 Fab; stroke; cerebroprotective; vasotropic;  
KW human; heavy chain.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN US2004057951-A1.  
XX  
PD 25-MAR-2004.  
XX  
PF 31-MAR-2003; 2003US-00404286.  
XX  
PR 23-JAN-1996; 96US-0093038P.  
PR 22-JAN-1997; 97US-00788800.  
PR 17-FEB-1999; 99US-00251652.  
PR 20-DEC-2000; 2000US-00811384.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Bednar MM, Gross CE, Thomas GR, Gross LJ;  
XX  
DR WPI; 2004-257111/24.  
XX  
PT Increasing cerebral blood flow and/or reducing infarct size in focal  
PT ischemic stroke caused by obstruction of a main cerebral artery in a  
PT human comprises co-administering tissue plasminogen activator and anti-  
PT CD18 antibody.  
XX  
PS Claim 11; SEQ ID NO 10; 26pp; English.  
XX  
CC The present invention relates to a method for increasing cerebral blood  
CC flow and/or reducing infarct size in focal ischaemic stroke caused by  
CC obstruction of a main cerebral artery in a mammal, particularly humans.  
CC The method comprises co-administering tissue plasminogen activator (tPA)

CC and anti-CD18 antibody to the mammal, where neither the tPA nor the anti-  
 CC CD18 antibody is administered to the mammal until about 3-5 hours after  
 CC the onset of focal ischemic stroke. The anti-CD18 antibody is a  
 CC humanised H52 antibody (huH52 Fab). The anti-CD18 antibody binds to an  
 CC extracellular domain of CD18 and inhibits or reduces the ability of a  
 CC cell expressing CD18 to bind to endothelium. The anti-CD18 antibody binds  
 CC CD18 with an affinity of 1-4 nm or less. The anti-CD18 antibody  
 CC dissociates the CD11b/CD18 complex. The anti-CD18 antibody binds to the  
 CC epitope bound by H52 antibody. The anti-CD18 antibody and the tPA are  
 CC simultaneously administered to the mammal, or the anti-CD18 antibody is  
 CC administered before the tPA is administered to the mammal. The method is  
 CC useful in increasing cerebral blood flow and/or reducing infarct size in  
 CC focal ischemic stroke caused by obstruction of a main cerebral artery in  
 CC a human. The antibodies are particularly useful for treating stroke.  
 CC Unlike previous methods, the new method of treatment does not require  
 CC prior administration of a thrombolytic agent to the mammal in order to  
 CC remove an embolus/thrombus, and therefore increases cerebral blood flow  
 CC and/or reduces infarct size. The present sequence represents the heavy  
 CC chain of huH52 Fab.

CC Sequence 232 AA;

Query Match 78.8%; Score 499.5; DB 8; Length 232;

Best Local Similarity 77.0%; Pred. No. 4,2e-39;

Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCATSGYTFEYTHHWROAPGKLEWVASINPDYDTNY 60

DB 1 EVOLVESGGGLVPGGSLRLSCATSGYTFEYTHHWROAPGKLEWVASINPDYDTNY 60

QY 61 NORFKGRFTISLDKSRRTAYLQNNSLRAEDTAVYYCASHIS-----DFDYWGQGLTV 113

DB 61 NORFKGRFTISLDKSRRTAYLQNNSLRAEDTAVYYCASHIS-----DFDYWGQGLTV 120

QY 114 TVSSAS 119

DB 121 TVSSAS 126

RESULT 6

AAW95614 ID AAW95614 standard; protein; 241 AA.

AAW95614;

08-JUN-1999 (first entry)

Humanized anti-CD18 antibody rhumAb CD18 heavy chain.

Monoclonal antibody; heavy chain; humanized; myocardial infarction;

burns; thermal injury; ischemic; shock; ischemic; haemorrhagic;

hemorrhagic; stroke.

Mus musculus.

Synthetic.

WO9856418-A1.

12-JUN-1998; 98WO-US0122209.

13-JUN-1997; 97US-00874897.

(GETH ) GENENTECH INC.

Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z, Wang SX;

Weisburg RP, Wong RU,

WPI; 1999-080860/07.

New stable aqueous antibody formulations - comprising an antibody not  
 subjected to lyophilisation, a buffer maintaining the pH at 4.5 - 6, a

PT surfactant and a polyol.

PS Disclosure; Fig 1A; 87pp; English.

CC The sequence is that of the heavy chain of a humanized murine anti-CD18

CC antibody rhumAb CD18. It can be used for the treatment of disorders which

CC include haemorrhagic shock, thermal injury (such as that resulting from

CC burns), stroke (including ischemic and hemorrhagic stroke) and

CC myocardial infarction. The antibody formulation can be stabilised at a

CC temperature of 2-8 deg. C for at least one year or at a temperature of 30

CC deg. C for at least one month and is stable following freezing and

CC thawing

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CC

QY 1 EVOLVESGGGLVPGGSLRLSCATSGYTFEYTHHWROAPGKLEWVASINPDYDTNY 60

DB 1 EVOLVESGGGLVPGGSLRLSCATSGYTFEYTHHWROAPGKLEWVASINPDYDTNY 60

QY 61 NORFKGRFTISLDKSRRTAYLQNNSLRAEDTAVYYCASHIS-----DFDYWGQGLTV 113

DB 61 NORFKGRFTISLDKSRRTAYLQNNSLRAEDTAVYYCASHIS-----DFDYWGQGLTV 120

QY 114 TVSSAS 119

DB 121 TVSSAS 126

RESULT 7

AAB66776 ID AAB66776 standard; protein; 241 AA.

AAB66776;

10-APR-2001 (first entry)

rhumAb CD18 heavy chain.

Antibody; lyophilization; hemorrhagic shock; thermal injury;

myocardial infarction; inflammation.

Homosapiens.

US6171586-B1.

09-JAN-2001.

12-JUN-1998; 98US-00097171.

13-JUN-1997; 97US-0053087P.

(GETH ) GENENTECH INC.

Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z, Wang SX;

Weisburg RP, Wong RU,

WPI; 2001-136863/14.

Stable aqueous pharmaceutical formulation for treating hemorrhagic shock,

thermal injury, stroke, and myocardial infarction, comprises an antibody

PT not subjected to prior lyophilization.

PS Example 1; Fig 1; 56pp; English.

CC The present invention relates to a stable aqueous pharmaceutical

CC formulation, comprising an antibody not subjected to prior

CC lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and a

CC polyol. The invention is useful for treating hemorrhagic shock, thermal

CC injury, e.g. resulting from burns, stroke including ischemic and



CC hemorrhagic stroke, myocardial infarction, inflammatory disorders such as  
 CC adult respiratory distress syndrome (ARDS), hypovolemic shock, ulcerative  
 CC colitis, rheumatoid arthritis and B-cell lymphomas  
 XX Sequence 241 AA;

Query Match 78.8%; Score 499.5; DB 4; Length 241;  
 Best Local Similarity 77.0%; Pred. No. 4,4e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRLSCATSGYTFETYYIHWRQAPKGLWVASINPDYDITNY 60  
 DB 1 EVOLVESGGGLVQPGSRLSCATSGYTFETYYHWRQAPKGLWVASINPDYDITNY 60  
 QY 61 NORPKGRFTISLDISKRTAVLYQNNSLRAEDTAVVYVCASWIS-----DFPDYWGQGLTV 113  
 DB 61 NORPKGRFTISLDISKRTAVLYQNNSLRAEDTAVVYVCASWIS-----DFPDYWGQGLTV 120  
 QY 114 TVSSAS 119  
 DB 121 TVSSAS 126

RESULT 8  
 AAW30631  
 ID AAW30631 standard; protein; 277 AA.

XX AAW30631;  
 XX 06-APR-1999 (first entry)

DE Recombinant humanised anti-CD18 antibody rhumab CD18 heavy chain.

XX Recombinant humanised anti-CD18 antibody; rhumab CD18; leucine zipper;  
 KW murine monoclonal antibody; mUMAB H52; protein recovery; filtration;  
 KW chromatography.

XX Mus sp.  
 OS Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Region 242..277  
 FT /label= leucine\_zipper

XX W09856808-A1.

XX 17-DEC-1998.

XX 12-JUN-1998; 98WO-US012334.

XX 13-JUN-1997; 97US-0050951P.

XX (GETH ) GENENTECH INC.

XX Blank GS, Narindray DS, Zapata GA;

XX WPI; 1999-060267/05.

XX New method for recovering polypeptides from cell cultures - by treating  
 PT with reagent and filtering to remove reagent.

XX Example; Fig 1A; 43pp; English.

XX A method has been developed for recovering a polypeptide comprising: (a)  
 CC exposing a composition comprising a polypeptide to a reagent which binds  
 CC to or modifies the polypeptide, where the reagent is immobilized on a  
 CC solid phase; and (b) passing the composition through a filter bearing an  
 CC opposite charge to the reagent so as to remove leached reagent from the  
 CC composition. The present invention also describes a method for modifying  
 CC a precursor antibody comprising a leucine zipper by exposing the  
 CC precursor antibody to a protease immobilized on a solid support so that  
 CC the protease removes the zipper. The method can be used to purify

CC proteins from cell cultures. They are especially useful for isolating  
 CC antibodies. The method overcomes the problem of reagent leakage into the  
 CC protein as is the case in prior art immobilized modification systems. By  
 CC using a opposite charge filter the reagent can be excluded from the  
 CC sample, preventing contamination. The present sequence represents the  
 CC recombinant humanised anti-CD18 antibody (rhumab CD18) heavy chain, which  
 CC is used in an example from the present invention

XX Sequence 277 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 277;  
 Best Local Similarity 77.0%; Pred. No. 5.1e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRLSCATSGYTFETYYIHWRQAPKGLWVASINPDYDITNY 60  
 DB 1 EVOLVESGGGLVQPGSRLSCATSGYTFETYYHWRQAPKGLWVASINPDYDITNY 60  
 QY 61 NORPKGRFTISLDISKRTAVLYQNNSLRAEDTAVVYVCASWIS-----DFPDYWGQGLTV 113  
 DB 61 NORPKGRFTISLDISKRTAVLYQNNSLRAEDTAVVYVCASWIS-----DFPDYWGQGLTV 120  
 QY 114 TVSSAS 119  
 DB 121 TVSSAS 126

RESULT 9  
 AAW95623  
 ID AAW95623 standard; protein; 300 AA.

XX AAW95623;  
 XX 08-JUN-1999 (first entry)

DE PS1130 expression cassette encoded rhumab CD18 heavy chain.

XX Monoclonal antibody; heavy chain; humanized; myocardial infarction;  
 KW burns; thermal injury; ischemic; shock; ischemic; hemorrhagic;  
 KW hemorrhagic; stroke; heavy chain.

XX Mus musculus.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Peptide 1..23

XX W09856418-A1.

XX 17-DEC-1998.

XX 12-JUN-1998; 98WO-US012209.

XX 13-JUN-1997; 97US-00874897.

XX (GETH ) GENENTECH INC.

XX Lam XM, Oeswein JQ, Ongpipatanakul B, Shahrokh Z, Wang SX;  
 PI Weisburg RP, Wong RL;

XX WPI; 1999-080860/07.

XX New stable aqueous antibody formulations - comprising an antibody not  
 PT subjected to lyophilisation, a buffer maintaining the pH at 4.5 - 6, a  
 PT surfactant and a polyol.

XX Disclosure; Fig 21A; 87pp; English.

XX The sequence is that of the PS1130 encoded heavy chain of a humanized  
 CC murine anti-CD18 antibody rhumab CD18. It can be used for the treatment of  
 CC disorders which include hemorrhagic shock, thermal injury (such as that  
 CC resulting from burns), stroke (including ischemic and hemorrhagic  
 CC stroke) and myocardial infarction. The antibody formulation can be

CC stabilised at a temperature of 2-8 deg. C for at least one year or at a  
CC temperature of 30 deg. C for at least one month and is stable following  
CC freezing and thawing  
XX

SO Sequence 300 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 300;  
Best Local Similarity 77.0%; Pred. No. 5.5e-39;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTEYIIHWRQAPGKGLRWASINPDYDITNY 60

DB 24 EVOLVESGGGLVPGGSLRLSCLATGTYFTEYIIHWRQAPGKGLRWASINPDYDITNY 83

QY 61 NORFKGRFTISLDKSKRTAYLQNNSLRAEDTAVYYCASWIS-----DFDYWGQGLTV 113

DB 84 NORFMDFRTISVDKSTSTAYMQNNSLRAEDTAVYYCARWRGLNGYGFVRFVWGQGLTV 143

QY 114 TVSSAS 119

DB 144 TVSSAS 149

RESULT 10

AAM30635  
ID AAM30635 standard; protein; 300 AA.

XX AAM30635;

DT 06-APR-1999 (first entry)

XX Recombinant humanised anti-CD18 antibody rhumab CD18 heavy chain.

KM Recombinant humanised anti-CD18 antibody; rhumab CD18; leucine zipper;

KW murine monoclonal antibody; mumab H52; protein recovery; filtration;

XX chromatography.

OS Mus sp.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..23

PN WO9856808-A1

PD 17-DEC-1998.

PF 12-JUN-1998; 98WO-US012334.

PR 13-JUN-1997; 97US-0050951P.

PA (GETH ) GENENTECH INC.

PI Blank GS, Narindray DS, Zapata GA;

DR WPI; 1999-060267/05.

DR N-PSDB; AAX03840.

PT New method for recovering polypeptides from cell cultures - by treating  
PT with reagent and filtering to remove reagent.

PS Example; Fig 4; 43pp; English.

XX A method has been developed for recovering a polypeptide comprising: (a)  
CC exposing a composition comprising a polypeptide to a reagent which binds  
CC to or modifies the polypeptide, where the reagent is immobilized on a  
CC solid phase; and (b) passing the composition through a filter bearing an  
CC opposite charge to the reagent so as to remove leached reagent from the  
CC composition. The present invention also describes a method for modifying  
CC a precursor antibody comprising a leucine zipper by exposing the  
CC precursor antibody to a protease immobilized on a solid support so that

CC the protease removes the zipper. The methods can be used to purify  
CC proteins from cell cultures. They are especially useful for isolating  
CC antibodies. The methods overcome the problem of reagent leakage into the  
CC protein as is the case in prior art immobilized modification systems. By  
CC using a opposite charge filter the reagent can be excluded from the  
CC sample, preventing contamination. The present sequence represents the  
CC recombinant humanised anti-CD18 antibody (rhumab CD18) heavy chain, which  
CC is used in an example from the present invention  
XX

SO Sequence 300 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 300;  
Best Local Similarity 77.0%; Pred. No. 5.5e-39;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTEYIIHWRQAPGKGLRWASINPDYDITNY 60

DB 24 EVOLVESGGGLVPGGSLRLSCLATGTYFTEYIIHWRQAPGKGLRWASINPDYDITNY 83

QY 61 NORFKGRFTISLDKSKRTAYLQNNSLRAEDTAVYYCASWIS-----DFDYWGQGLTV 113

DB 84 NORFMDFRTISVDKSTSTAYMQNNSLRAEDTAVYYCARWRGLNGYGFVRFVWGQGLTV 143

QY 114 TVSSAS 119

DB 144 TVSSAS 149

RESULT 11

AAB66785  
ID AAB66785 standard; protein; 300 AA.

XX AAB66785;

DT 10-APR-2001 (first entry)

XX Protein encoded by ps 1130 expression cassette.

KM Antibody; lyophilization; hemorrhagic shock; thermal injury;

KW myocardial infarction; inflammation.

XX Homo sapiens.

XX US6171586-B1.

PD 09-JAN-2001.

PF 12-JUN-1998; 98US-00097171.

PR 13-JUN-1997; 97US-0053087P.

PA (GETH ) GENENTECH INC.

PI Lam XM, Oeswein JO, Ongpipattanakul B, Shahrokh Z, Wang SX;

PI Weisburg RP, Wong RL;

DR WPI; 2001-136863/14.

PT Stable aqueous pharmaceutical formulation for treating hemorrhagic shock,  
PT thermal injury, stroke, and myocardial infarction, comprises an antibody  
PT not subjected to prior lyophilization.

PS Disclosure; Fig 21; 56pp; English.

XX The present invention relates to a stable aqueous pharmaceutical  
CC formulation, comprising an antibody not subjected to prior  
CC lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and a  
CC polyol. The invention is useful for treating hemorrhagic shock, thermal  
CC injury, e.g. resulting from burns, stroke including ischemic and  
CC hemorrhagic stroke, myocardial infarction, inflammatory disorders such as  
CC adult respiratory distress syndrome (ARDS), hypovolemic shock, ulcerative  
CC colitis, rheumatoid arthritis and B-cell lymphomas  
XX

SQ Sequence 300 AA;  
 Query Match 78.8%; Score 499.5; DB 4; Length 300;  
 Best Local Similarity 77.0%; Pred. No. 5.5e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYPTEYIIHWVQAQPKGLEWVASINPDYDITNY 60  
 DB 24 EVQLVESGGGLVQPGGSLRLSCATGYPTEYIIHWVQAQPKGLEWVASINPDYDITNY 83  
 QY 61 NQRFKGRFTISLDKSKRTAYLQWNSLRADTAIVYVCASWIS-----DFPDYWGQGTLY 113  
 DB 84 NQRFMDRFTISVDKSTSTAYVQWNSLRADTAIVYVCARMRGLANYGPDVRYPDVWGQGTLY 143  
 QY 114 TVSSNS 119  
 DB 144 TVSSNS 149

RESULT 12  
 ABP72746  
 ID ABP72746 standard; protein; 300 AA.  
 AC ABP72746;  
 XX  
 DT 11-JUN-2003 (first entry)  
 DE Anti-CD18 antibody heavy chain-leucine zipper.  
 XX  
 KM CD18; antibody; heavy chain; pxCd18-7T3; immunosuppressive.  
 XX  
 OS Unidentified.  
 OS Escherichia coli.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..23  
 FT /label= Signal peptide  
 FT /note= "heat stable enterotoxin II (STII) signal"  
 FT Protein 24..300  
 FT /note= "Heavy chain-leucine zipper"  
 XX  
 PN WO2003018771-A2.  
 PD 06-MAR-2003.  
 PF 26-AUG-2002; 2002WO-US027220.  
 XX  
 PR 27-AUG-2001; 2001US-0315209P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Andersen DC, Simmons LC,  
 XX  
 DR WPI, 2003-278654/27.  
 DR N-PSDB; AB282071.  
 XX  
 PT Producing an antibody for treating cancer or autoimmune diseases by  
 PT culturing the host cell under suitable conditions so that the light chain  
 PT and heavy chain are expressed in a sequential fashion.  
 XX  
 PS Claim 52, Fig 3, 73pp; English.  
 XX  
 CC The present sequence is that of an anti-CD18 antibody heavy chain  
 CC including a heat stable enterotoxin II (STII) secretion signal and a C-  
 CC terminal leucine zipper domain. This recombinant heavy chain is produced  
 CC by host cells transformed with claimed vector pxCd18-7T3 (see AB282071).  
 CC The plasmid contains 2 translational units that temporally separate the  
 CC transcription of the light chain (see ABP72745) and heavy chains.  
 CC Expression of the light chain is under the control of the phoA promoter,  
 CC while expression of the heavy chain is under the control of the inducible  
 CC TacI promoter. In an example from the invention, Escherichia coli 59A7  
 CC was transformed with pxCd18-7T3. The light chain was expressed initially

CC and secreted into the periplasmic space. Heavy chain production was then  
 CC induced by addition of IPTG, and F(ab')<sub>2</sub> assembly occurred almost  
 CC immediately. A yield of 4.6 +/- 0.5 g/l assembly obtained using a single promoter  
 CC nearly 2-fold increase on the yield obtained using a single promoter  
 CC system. This is an example of the process of the invention for production  
 CC of recombinant antibodies in a host cell system, with temporally  
 CC separated expression of the light and heavy chains. Properly assembled,  
 CC soluble and functional antibodies (or their fragments) can be produced in  
 CC high yields for diagnostic or therapeutic applications, including  
 CC treatment of cancer or autoimmune diseases

SQ Sequence 300 AA;  
 Query Match 78.8%; Score 499.5; DB 6; Length 300;  
 Best Local Similarity 77.0%; Pred. No. 5.5e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYPTEYIIHWVQAQPKGLEWVASINPDYDITNY 60  
 DB 24 EVQLVESGGGLVQPGGSLRLSCATGYPTEYIIHWVQAQPKGLEWVASINPDYDITNY 83  
 QY 61 NQRFKGRFTISLDKSKRTAYLQWNSLRADTAIVYVCASWIS-----DFPDYWGQGTLY 113  
 DB 84 NQRFMDRFTISVDKSTSTAYVQWNSLRADTAIVYVCARMRGLANYGPDVRYPDVWGQGTLY 143  
 QY 114 TVSSNS 119  
 DB 144 TVSSNS 149

RESULT 13  
 AAW34505  
 ID AAW34505 standard; protein; 450 AA.  
 AC AAW34505;  
 XX  
 DT 19-MAR-1998 (first entry)  
 DE Heavy chain of full length IgG2 humanised H52 antibody.  
 XX  
 KM Humanised antibody; Huh52; heavy chain; focal ischaemic stroke; embolism;  
 KM brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;  
 KM transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;  
 KM systemic hypoperfusion; cardiac arrest.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 OS Mus sp.  
 XX  
 PN WO9726912-A2.  
 PD 31-JUL-1997.  
 PF 11-JAN-1997; 97WO-US000492.  
 XX  
 PR 23-JAN-1996; 96US-00589982.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
 XX  
 PI Bednar MM, Grose CE, Thomas GR;  
 XX  
 DR WPI, 1997-393373/36.  
 DR  
 XX  
 PT Administering an anti-CD18 antibody to treat focal ischaemic stroke - by  
 PT increasing cerebral blood flow and reducing size of brain infarct.  
 XX  
 PS Disclosure; Page 9, 41pp; English.  
 XX  
 CC This sequence represents the heavy chain of the humanised H52 antibody.  
 CC The H52 antibody can be used in the method of the invention. The method  
 CC is for treating focal ischaemic stroke, i.e. damage to the brain due to  
 CC interrupted blood supply, in a mammal, caused by obstruction of a main

CC cerebral artery, comprises administering anti-CD18 antibody to increase  
 CC cerebral blood flow and/or reduce the size of the area of brain that  
 CC dies, without removing the arterial obstruction. CD18, is upregulated in  
 CC patients after ischaemic stroke or transient ischaemic attack (stroke  
 CC symptoms last less than 24 hours with complete recovery). Treatment with  
 CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain  
 CC infarct size, improving clinical outcomes in focal ischaemic strokes in  
 CC mammals, particularly in humans. The method provides an alternative to  
 CC thrombolytic therapy for treating ischaemic strokes caused by  
 CC thromboembolism (thrombosis or embolism), particularly where thrombolytic  
 CC therapy has been unsuccessful, is contra-indicated e.g. because such  
 CC drugs exacerbate bleeding, or is unsuitable because of the time delay  
 CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue  
 CC plasminogen activator) may also be administered before, after or  
 CC simultaneously with the anti-CD18 antibody. Alternatively, the method can  
 CC be used to treat the third main type of ischaemic stroke, systemic  
 CC hypoperfusion, e.g. resulting from cardiac arrest or drowning

XX Sequence 450 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 450;  
 Best Local Similarity 77.0%; Pred. No. 8.6e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYYIHVWRQAPGKLEWVASINPDYDITNY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYYTMHWRQAPGKLEWVAGINPKNGGTSH 60  
 QY 61 NORPKGRFTISLDKSKRTAYLQNSLRAPETAVYYCASWIS-----DFPDYWGQSTLV 113  
 DB 61 NORPKGRFTISLDKSKRTAYLQNSLRAPETAVYYCARMRGLNYGPDVRYFDVWGQSTLV 120

QY 114 TVSSAS 119  
 DB 121 TVSSAS 126

RESULT 14  
 AAY08755  
 ID AAY08755 standard; protein; 450 AA.

AC AAY08755;  
 XX  
 DT 10-AUG-1999 (first entry)  
 XX  
 DE Human IgG2 huH52 heavy chain protein fragment.

XX  
 KW IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;  
 KW IgG4; kappa-CL domain; lambda-CL domain; focal ischaemic stroke;  
 KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;  
 KW CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;  
 KW antibody; huH52; heavy chain.

OS Homo sapiens.  
 XX  
 PN US5914112-A.  
 XX  
 PD 22-JUN-1999.  
 XX  
 PF 22-JAN-1997; 97US-00788800.  
 XX  
 PR 23-JAN-1996; 96US-0093038P.

XX  
 PA (GETH ) GENENTECH INC.  
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

XX Thomas GR, Bednar MM, Gross CE;

XX WPI; 1999-370483/31.

XX Anti-CD18 antibodies in stroke.

PS Disclosure; Col 31-34; 25pp; English.

XX This invention describes a method for improving the clinical outcome in  
 CC focal ischaemic stroke by administering novel anti-CD18 antibody which  
 CC has cerebroprotective properties. The invention particularly describes a  
 CC method of treating focal ischaemic stroke caused by the obstruction of a  
 CC main cerebral artery which comprises administering an anti-CD18 antibody  
 CC to increase the blood flow or reduce the infarct size, where: (1) the  
 CC antibody binds to an extracellular domain of CD18 and inhibits or reduces  
 CC the ability of the cell expressing CD18 to bind to endothelium, (2) the  
 CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the  
 CC antibody dissociates CD11b/CD18 complex. This sequence represents the  
 CC human IgG 2 huH52 heavy chain region

XX Sequence 450 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 450;  
 Best Local Similarity 77.0%; Pred. No. 8.6e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYYIHVWRQAPGKLEWVASINPDYDITNY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYYTMHWRQAPGKLEWVAGINPKNGGTSH 60  
 QY 61 NORPKGRFTISLDKSKRTAYLQNSLRAPETAVYYCASWIS-----DFPDYWGQSTLV 113  
 DB 61 NORPKGRFTISLDKSKRTAYLQNSLRAPETAVYYCARMRGLNYGPDVRYFDVWGQSTLV 120

QY 114 TVSSAS 119  
 DB 121 TVSSAS 126

RESULT 15  
 ABG31890  
 ID ABG31890 standard; peptide; 450 AA.

AC ABG31890;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX

DE Full length humanised H52 antibody (huH52), heavy chain.

XX  
 KW Human; humanised H52 antibody; huH52; cerebral blood flow; infarct size;  
 KW focal ischaemic stroke; main cerebral artery;  
 KW tissue plasminogen activator; anti-CD18 antibody; stroke;  
 KW acute ischaemic stroke; thrombolytic therapy;  
 KW Fabryb salvage receptor binding epitope; thromboembolic stroke.

OS Homo sapiens.  
 XX  
 PN US2002081294-A1.

XX  
 PD 27-JUN-2002.

XX  
 PF 20-DEC-2000; 2000US-00811384.

XX  
 PR 23-JAN-1996; 96US-0093038P.

XX  
 PR 22-JAN-1997; 97US-00788800.

XX  
 PR 17-FEB-1999; 99US-00251652.

XX  
 PA (GETH ) GENENTECH INC.

XX  
 PI Bednar MM, Gross CE, Thomas GR, Gross LJ;

XX  
 DR WPI; 2002-626528/67.

XX Increasing cerebral blood flow and/or reducing infarct size in focal  
 PT ischaemic stroke using anti-CD18 antibody and tissue plasminogen activator  
 XX is useful to improve clinical outcome in acute ischemic stroke.

PS Disclosure; Page 6; 27pp; English.

CC The invention relates to a method of increasing cerebral blood flow and/  
 CC or reducing infarct size in focal ischaemic stroke caused by obstruction  
 CC of a main cerebral artery in a human, comprising co-administering tissue  
 CC plasminogen activator and anti-CD18 antibody about 3-5 hours after the  
 CC stroke. The method is used to improve the clinical outcome in acute  
 CC ischaemic stroke and to provide an alternative to thrombolytic therapy  
 CC for treating thromboembolic stroke, particularly where thrombolytic  
 CC therapy has been unsuccessful or is contra-indicated. The present  
 CC sequence represents the full length humanised H52 antibody (huH52), heavy  
 CC chain used in the method of the invention

XX  
 SQ Sequence 450 AA;

Query Match 78.8%; Score 499.5; DB 5; Length 450;  
 Best local Similarity 77.0%; Pred. No. 8,6e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIMHVRQAPGKGLWVASINPDYDITNY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIMHVRQAPGKGLWVASINPDYDITNY 60  
 QY 61 NORFKGRTISLIDSKRTAYLQMSLRADTAIVYCAWIS-----DFPDYWGQGLTV 113  
 DB 61 NORFMDRPTISVDKSTAYMQMSLRADTAIVYCAWRGILNGFDVRYEFDVWGQGLTV 120  
 QY 114 TVSSAS 119  
 DB 121 TVSSAS 126

Search completed: December 29, 2004, 19:35:44  
 Job time : 125.575 secs

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